

# Medicina Personalizada. Aplicaciones clínicas de las tecnologías ómicas

## Genómica

Valencia, 16 Jun 2015



PRINCIPE FELIPE  
CENTRO DE INVESTIGACION

Computational • Genomics



# Objetivos

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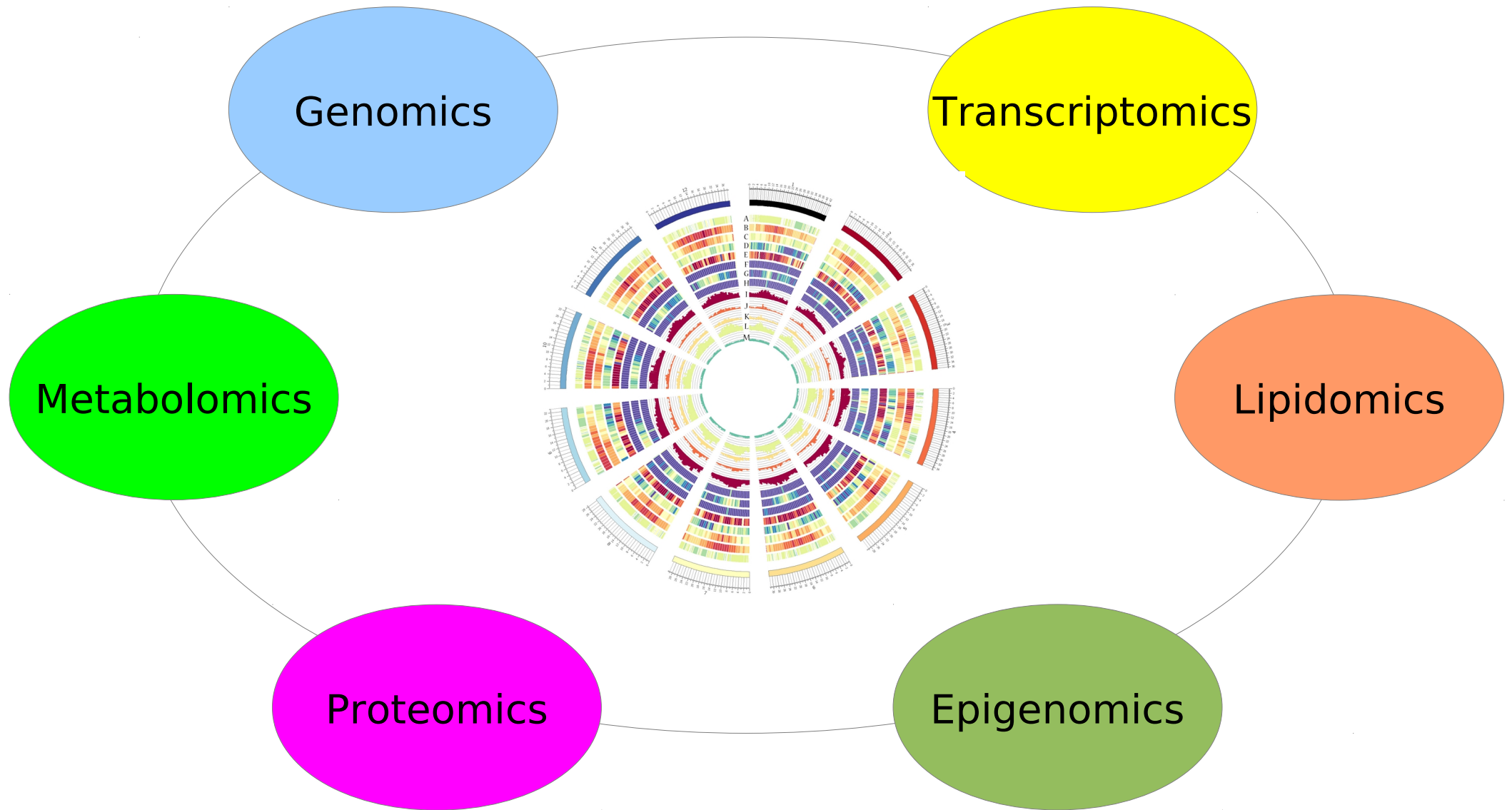
- **Generales**

- 1) Fomentar el conocimiento de las **tecnologías ómicas** entre los especialistas **clínicos**
- 2) Identificar **áreas terapéuticas de interés**
- 3) Facilitar el desarrollo de proyectos **multidisciplinares** basados en estas tecnologías

- **Específicos**

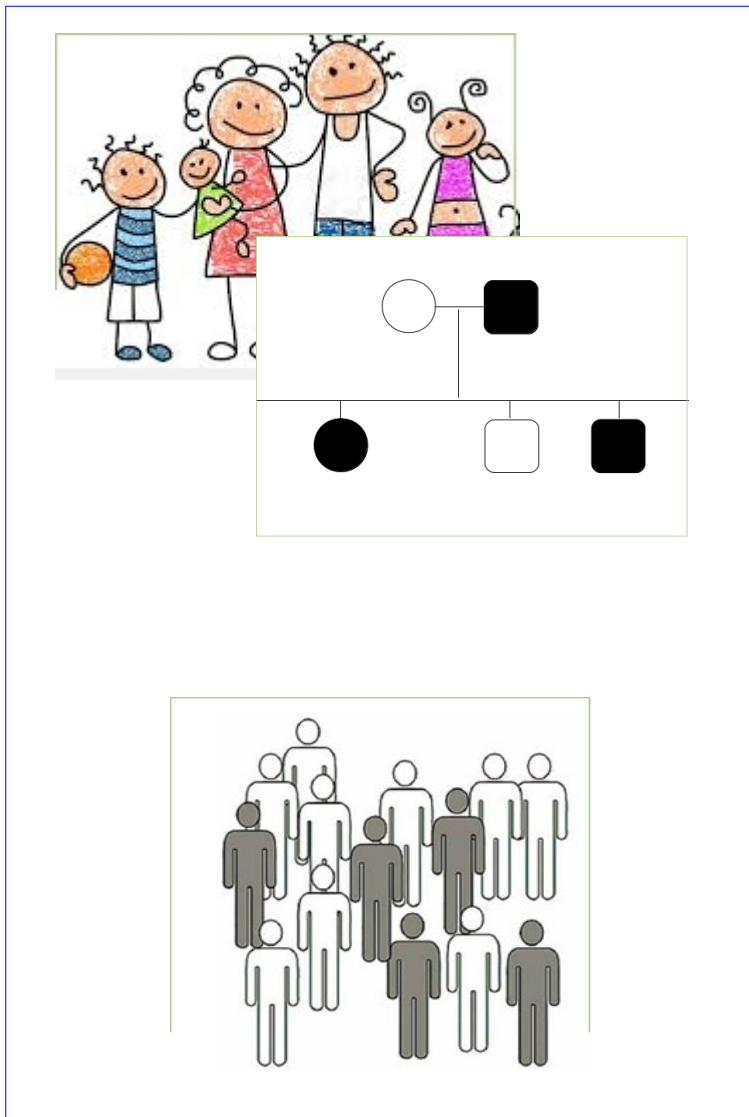
- 1) Dar a conocer a los profesionales sanitarios las posibilidades que las tecnologías ómicas ofrecen a nivel de **investigación y actividad asistencial**
- 2) Enseñar a los profesionales sanitarios a **diseñar protocolos y estrategias** que les permitan emplear estas tecnologías en sus proyectos de investigación y eventualmente en la práctica clínica
- 3) **Analizar e interpretar los resultados obtenidos** mediante estas tecnologías

# OMICS



**Medicina Personalizada:**  
**Aplicaciones clínicas de las tecnologías ómicas**

# Aplicaciones clínicas





# Outline

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## 1) Introduction to NGS Data Analysis

## 2) RNA-Seq Data Analysis

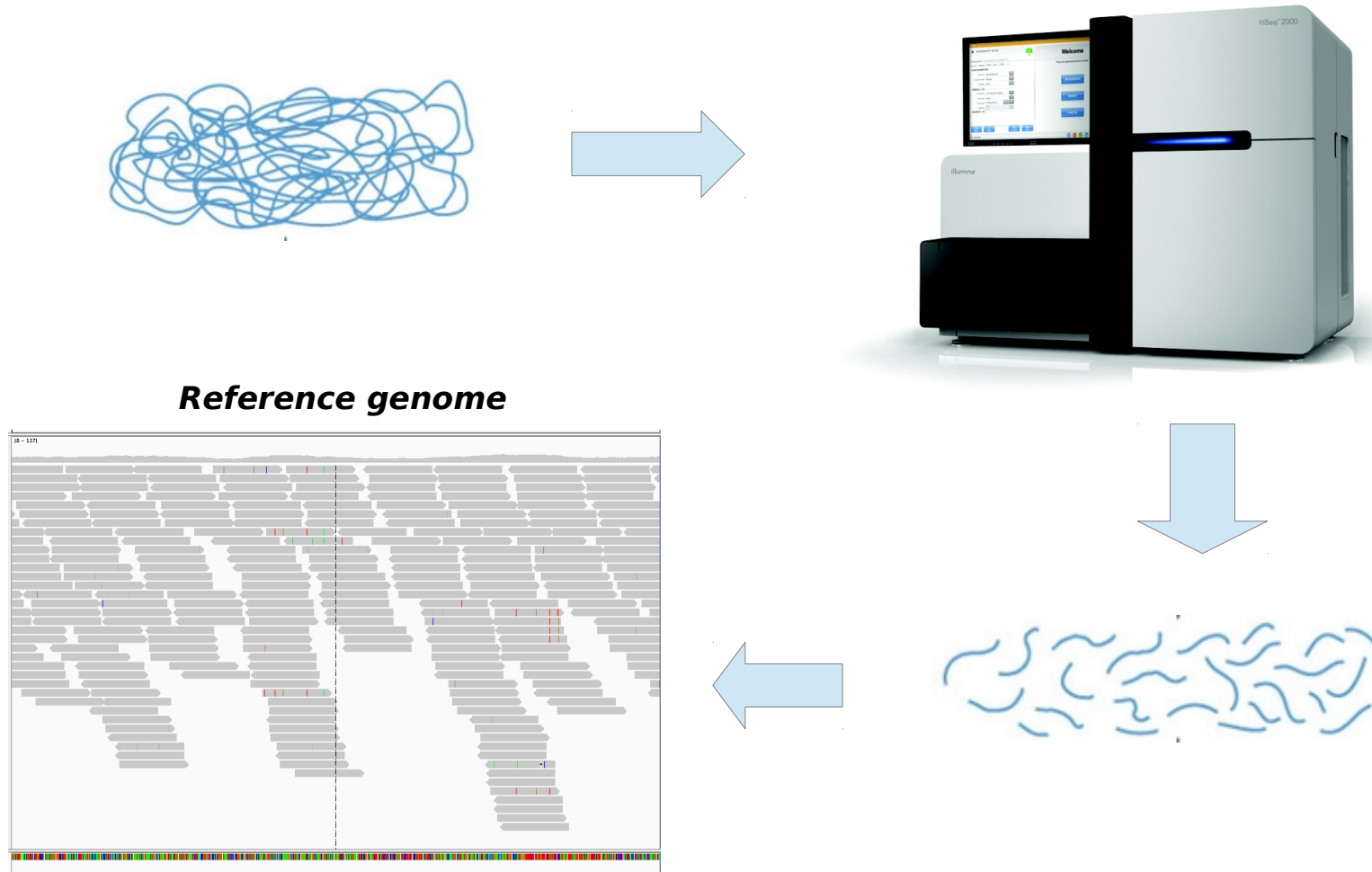
## 3) Resequencing Data Analysis

## 4) Omics Data Integration

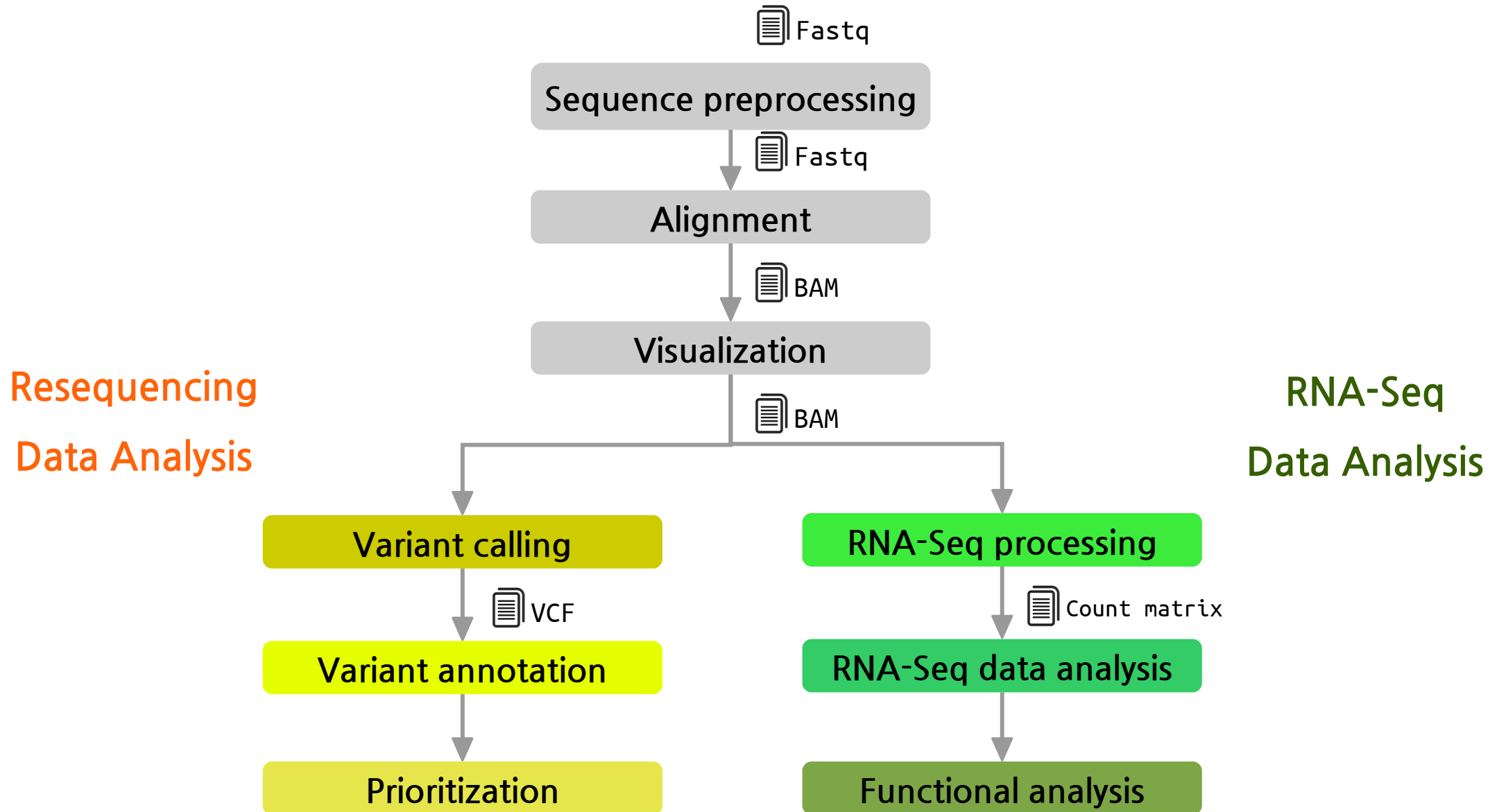
## 5) Network Analysis

# NGS technologies

How do these technologies work ?



# NGS Data Analysis Pipeline



# Fastq format

- We could say “it is a fasta with **qualities**”:
  - 1. Header (like the fasta but starting with “@”)
  - 2. Sequence (string of nt)
  - 3. “+” and sequence ID (optional)
  - 4. Encoded quality of the sequence

```
@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
+
!''*(((((***+))%%%+)(%%%) .1***-+*''))**55CCF>>>>>CCCCCCC65
```

# BAM/SAM format

```
@PG ID:HPG-Aligner VN:1.0
@SQ SN:20 LN:63025520

HWI-ST700660_138:2:2105:7292:79900#2@0/1 16 20 76703 254 76= * 0 0
GTTTAGATACTGAAAGGTACATACTTCTTTGTAGGAACAAGCTATCATGCTGCATTTCTATAATATCACATGAATA
GIJGJLGGFLILGGIEIFEKEDELIGLJIHJFIKKFELFIKLFFGLGHKKGJLFIIGKFFEFFEFGKCKFHHCCCF AS:i:254 NH:i:1 NM:i:0

HWI-ST700660_138:2:2208:6911:12246#2@0/1 16 20 76703 254 76= * 0 0
GTTTAGATACTGAAAGGTACATACTTCTTTGTAGGAACAAGCTATCATGCTGCATTTCTATAATATCACATGAATA
HHJFHLGFFLILEGIKIEEMGEDLIGLHIHJFIKKFELFIKLEFGKGHEKHJLFHIGKFFDFFEFGKDKFHHCCCF AS:i:254 NH:i:1 NM:i:0

HWI-ST700660_138:2:1201:2973:62218#2@0/1 0 20 76655 254 76M * 0 0
AACCCCAAAAATGTTGGAAGAATAATGTAGGACATTGCAGAAGACGATGTTTAGATACTGAAAGGGACATACTTCT
FEFFGHHHGGHFKCCJKFHIGIFFIFLDEJKGJGGFKIHLFIJGIEGFLDEDFLGEIIMHHIKL$BBGFFJIEHE AS:i:254 NH:i:1 NM:i:1

HWI-ST700660_138:2:1203:21395:164917#2@0/1 256 20 68253 254 4M1D72M * 0 0
NCACCCATGATAGACCAGTAAAGGTGACCACTTAAATTCCTTGCTGTGCAGTGTTCTGTATTCCTCAGGACACAGA
#4@ADEHFJFFEJDHJGKEFIHGHGBGFHHFIICEIIFFKIFHEGJEHHGLELEGKJMFGGGLEIKHLFGKIKHDG AS:i:254 NH:i:3 NM:i:1

HWI-ST700660_138:2:1105:16101:50526#6@0/1 16 20 126103 246 53M4D23M * 0 0
AAGAAGTGCAAACCTGAAGAGATGCATGTAAAGAATGGTTGGGCAATGTGCGGCAAAGGGACTGCTGTGTTCCAGC
FEHIGGHIGIGJI6FCFHJIFFLJJCJGJHGFKKKKGJIKHFFKIFFFKHFLKHGKJLJGKILLEFFLIHJIEIB AS:i:368 NH:i:1 NM:i:4
```

## SAM Specification:

<http://samtools.sourceforge.net/SAM1.pdf>

# VCF format

```
#fileformat=VCFv4.1
##fileDate=20090805
##source=myImputationProgramV3.1
##reference=file:///seq/references/1000GenomesPilot-NCBI36.fasta
##contig=<ID=20,length=62435964,assembly=B36,md5=f126cdf8a6e0c7f379d618ff66beb2da,species="Homo sapiens",taxonomy=x>
##phasing=partial
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##INFO=<ID=AF,Number=A,Type=Float,Description="Allele Frequency">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP membership, build 129">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FILTER=<ID=q10,Description="Quality below 10">
##FILTER=<ID=s50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT NA00001 NA00002 NA00003
20 14370 rs6054257 G A 29 PASS NS=3;DP=14;AF=0.5;DB;H2 GT:GQ:DP:HQ 0|0:48:1:51,51 1|0:48:8:51,51 1/1:43:5:.,.
20 17330 . T A 3 q10 NS=3;DP=11;AF=0.017 GT:GQ:DP:HQ 0|0:49:3:58,50 0|1:3:5:65,3 0/0:41:3
20 1110696 rs6040355 A G,T 67 PASS NS=2;DP=10;AF=0.333,0.667;AA=T;DB GT:GQ:DP:HQ 1|2:21:6:23,27 2|1:2:0:18,2 2/2:35:4
20 1230237 . T . 47 PASS NS=3;DP=13;AA=T GT:GQ:DP:HQ 0|0:54:7:56,60 0|0:48:4:51,51 0/0:61:2
20 1234567 microsat1 GTC G,GTCT 50 PASS NS=3;DP=9;AA=G GT:GQ:DP 0/1:35:4 0/2:17:2 1/1:40:3
```

<http://www.1000genomes.org/>

# Counts

Gene

Sample



Ensembl	Gene.Name	T1	T2	T3	T4	T5	WT1	WT2	WT3	WT4	WT5	WT6
ENSMUSG00000000134	Tfe3	312	295	333	258	392	257	344	223	423	277	389
ENSMUSG00000000142	Axin2	165	171	138	166	203	170	172	119	203	147	178
ENSMUSG00000000148	Brat1	213	196	207	224	350	204	268	143	300	177	288
ENSMUSG00000000149	Gna12	684	684	613	545	900	496	672	426	1023	583	797
ENSMUSG00000000154	Slc22a18	3	2	3	2	2	3	3	2	1	1	3
ENSMUSG00000000157	Itgb2l	0	0	0	0	0	0	0	0	0	0	0
ENSMUSG00000000159	Igsf5	0	0	0	0	0	0	0	0	0	0	0
ENSMUSG00000000167	Pih1d2	15	19	6	10	9	5	5	5	7	6	6
ENSMUSG00000000168	Dlat	899	777	967	756	1116	777	1047	614	1155	894	1126
ENSMUSG00000000171	Sdhd	1055	1003	1047	914	1430	939	1192	766	1390	916	1412
ENSMUSG00000000182	Fgf23	1	0	3	1	0	2	0	2	2	0	0
ENSMUSG00000000183	Fgf6	0	0	0	0	0	0	0	1	0	0	0
ENSMUSG00000000184	Ccnd2	1961	1978	1804	1779	2090	1655	2148	1585	2504	1895	2274
ENSMUSG00000000194	Gpr107	784	733	667	615	889	654	818	483	1034	627	1015
ENSMUSG00000000197	Nalcn	1120	1009	1047	917	1356	1129	1202	758	1625	1127	1044



# Outline

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1) Introduction to NGS Data Analysis

**2) RNA-Seq Data Analysis**

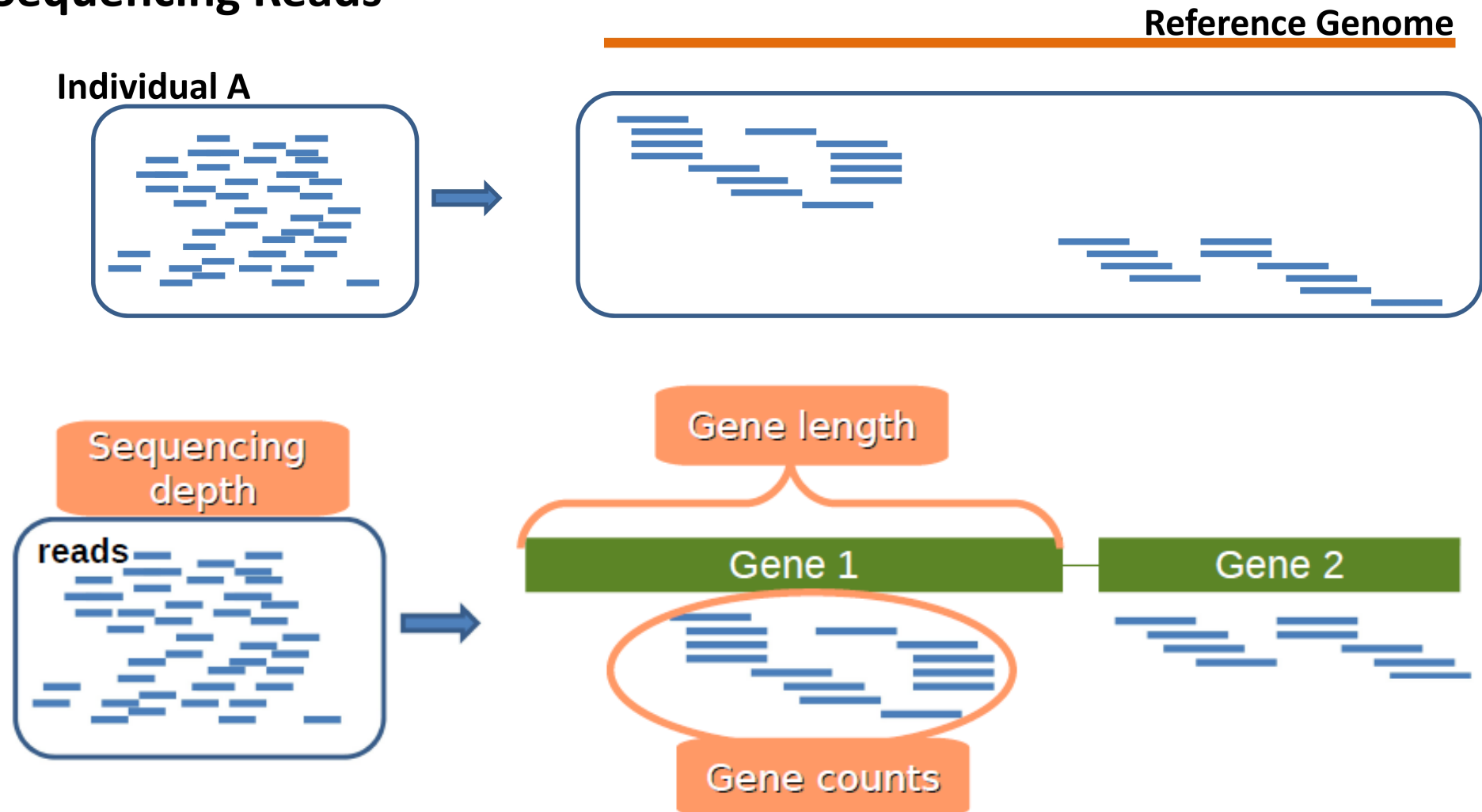
3) Resequencing Data Analysis

4) Omics Data Integration

5) Network Analysis

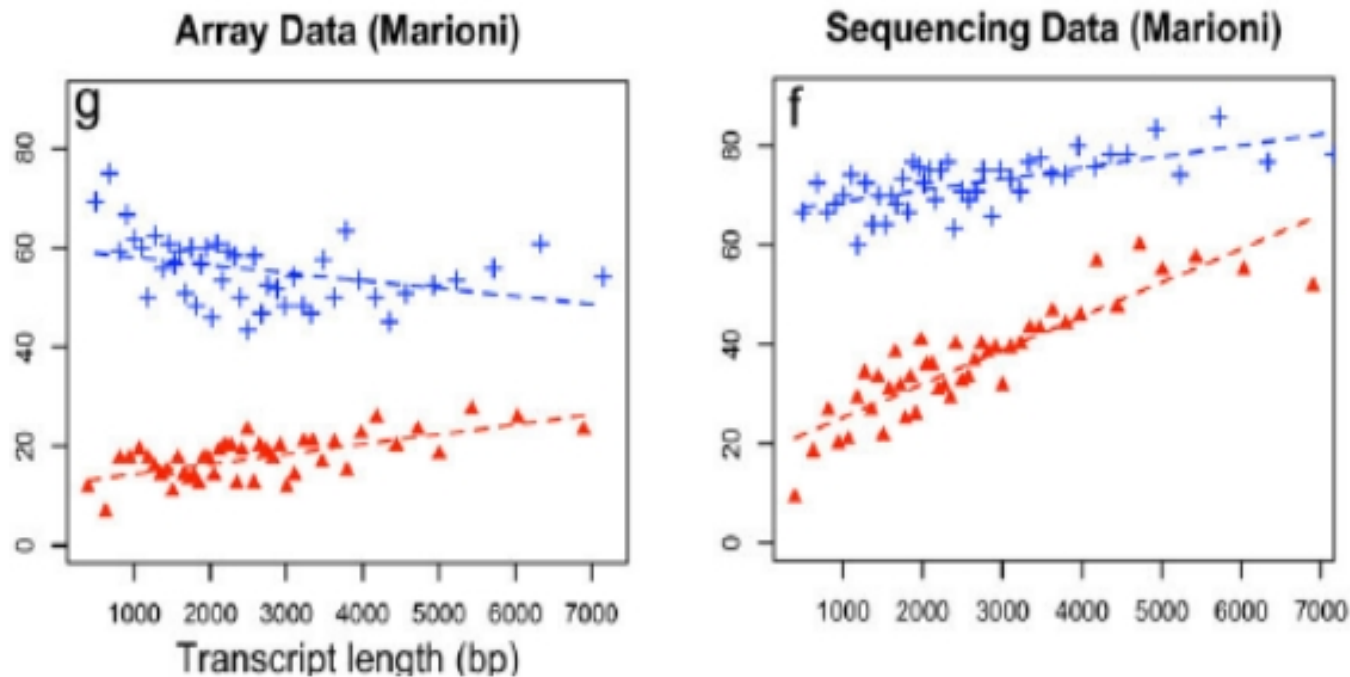
# General context

## Sequencing Reads



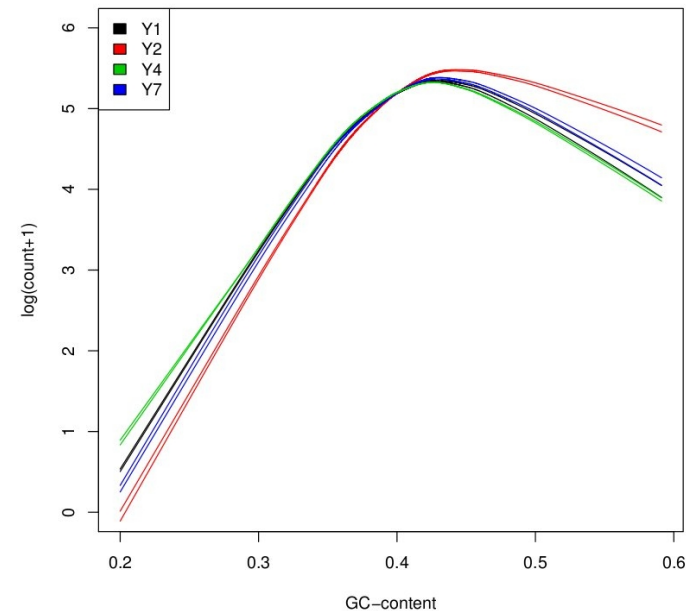
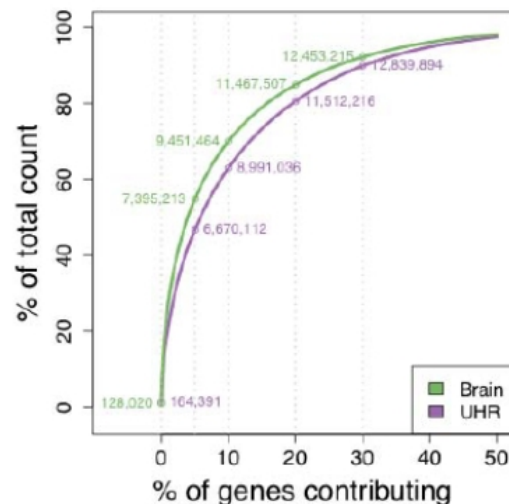
# Gene/transcript length dependence

- Counts are proportional to...
  - the transcript length
  - the mRNA expression level.



# Count Normalization

- **Transcript length:** *within* library
- **Library size:** *between* libraries
- Many **other biases** ...
  - ▢ Differences on the read count distribution among samples.
  - ▢ GC content of the gene affects the detection of that gene (Illumina)
  - ▢ sequence-specific bias is introduced during the library preparation



# Count Normalization

- **RPKM**: Reads Per Kilobase of the transcript per Million mapped reads

$$RPKM = 10^9 \times \frac{C}{N * L}$$

- **C** is the number of mappable reads mapped onto the gene's exons.
- **N** is the total number of mappable reads in the experiment.
- **L** is the total length of the exons in base pairs.
- Fragments Per Kilobase of exon per Million fragments mapped (FPKM),

# RNA-Seq Data Analysis Pipeline

Primary

1. Sequence preprocessing



2. Mapping



3. Quantification

Secondary

4. Normalization



5. Differential expression



6. Functional Profiling





# Babelomics 5

Plataforma de análisis de  
datos de Transcriptómica, Proteómica  
y Genómica con diferentes abordajes  
funcionales

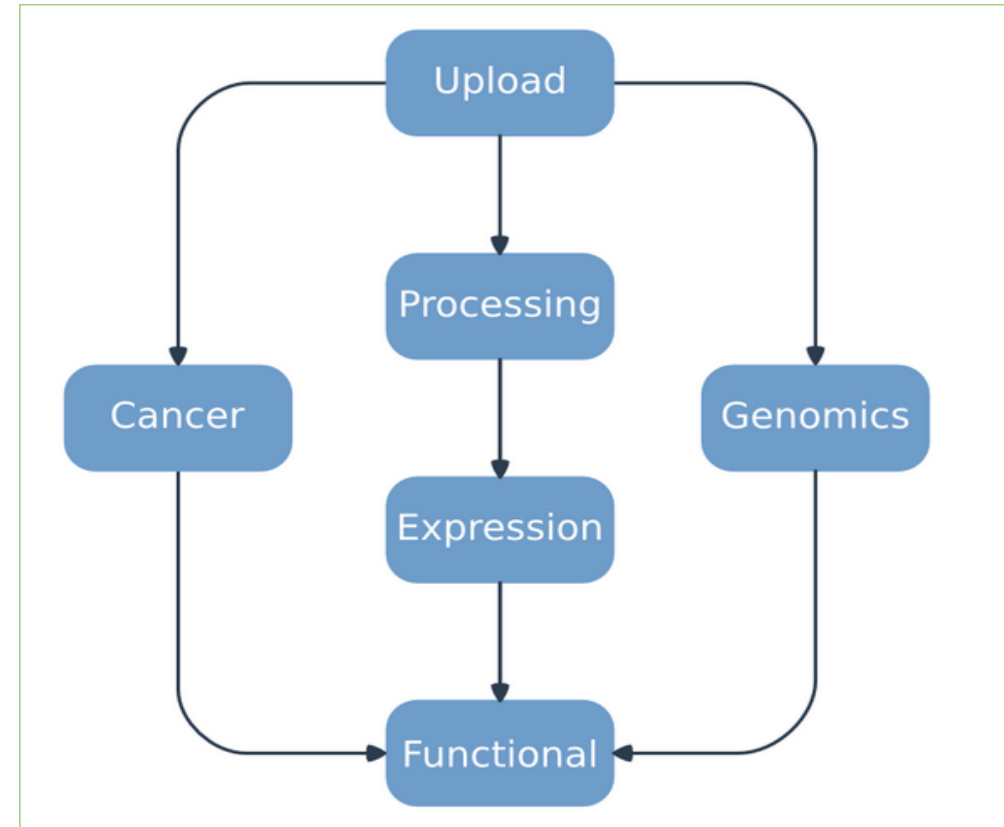
<http://babelomics.bioinfo.cipf.es/>



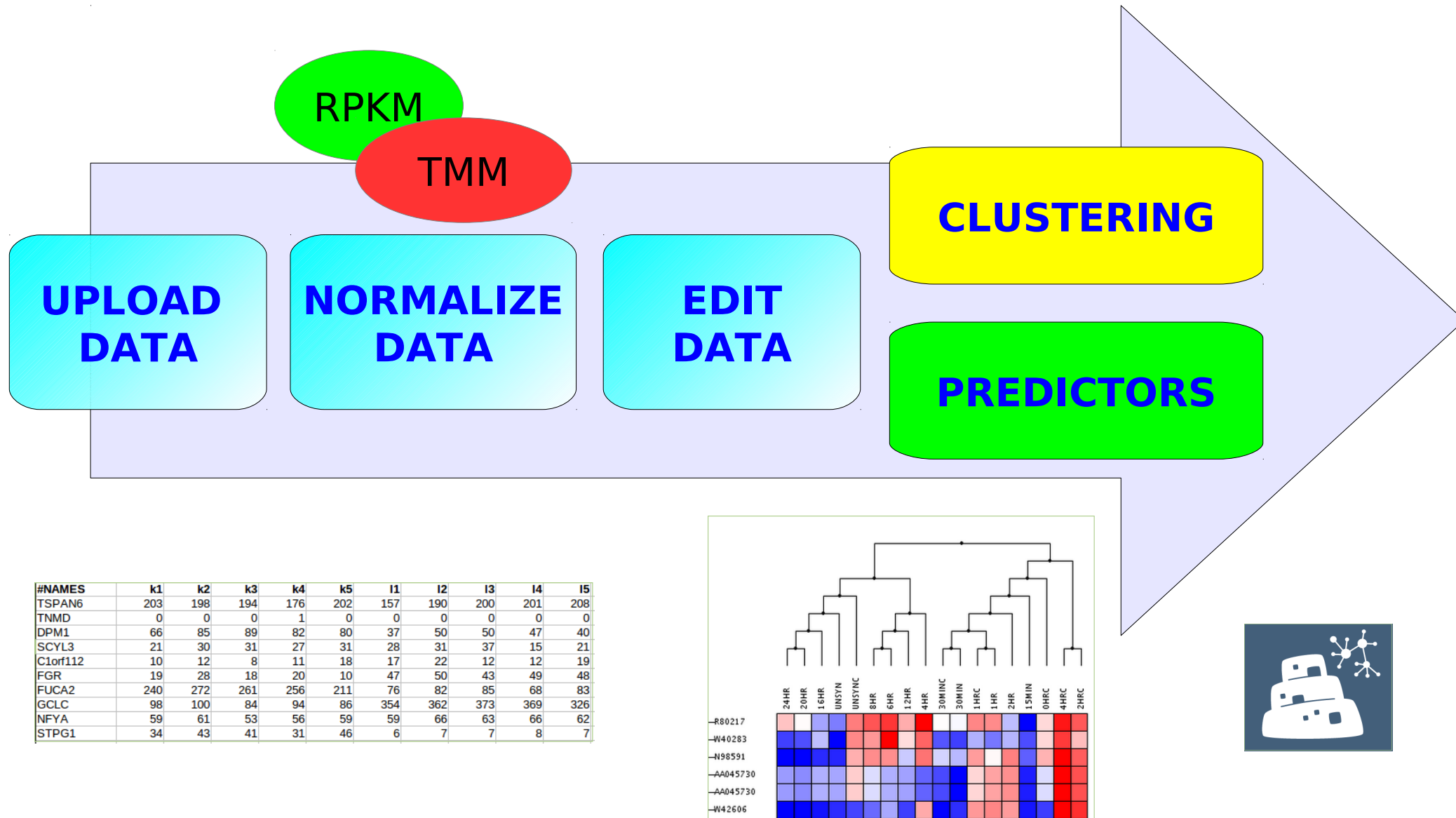
# Tool interface

## Babelomics 5

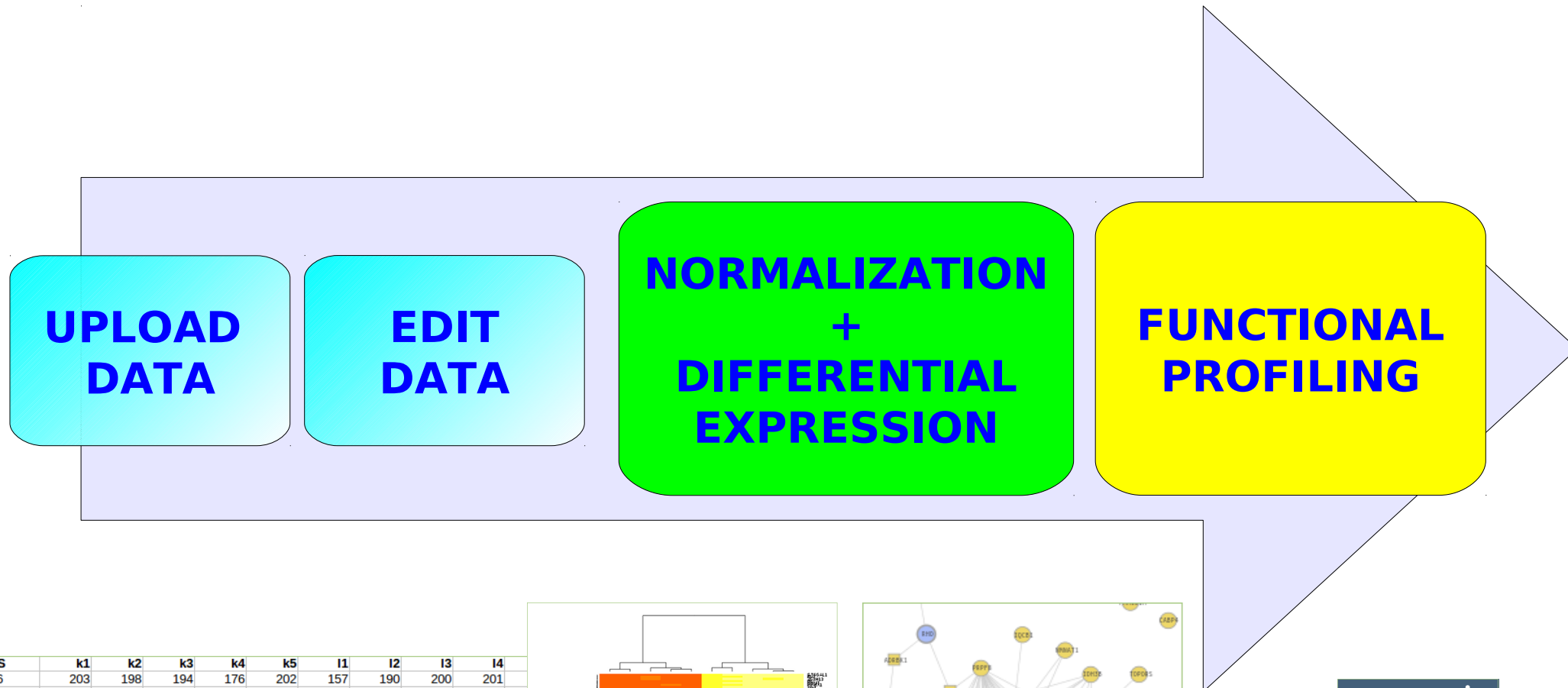
GENE EXPRESSION, GENOME  
VARIATION AND FUNCTIONAL  
PROFILING ANALYSIS SUITE



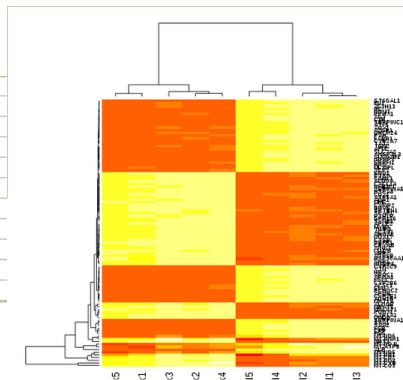
# Supervised and Unsupervised Classification



# Differential Expression



#NAMES	k1	k2	k3	k4	k5	l1	l2	l3	l4
TSPAN6	203	198	194	176	202	157	190	200	201
TNMD	0	0	0	1	0	0	0	0	0
DPM1	66	85	89	82	80	37	50	50	47
SCYL3	21	30	31	27	31	28	31	37	15
C1orf112	10	12	8	11	18	17	22	12	12
FGR	19	28	18	20	10	47	50	43	49
FUCA2	240	272	261	256	211	76	82	85	68
GCLC	98	100	84	94	86	354	362	373	369
NFYA	59	61	53	56	59	59	66	63	66
STPG1	34	43	41	31	46	6	7	7	8



# Hands on



## Babelomics 5

<http://babelomics.bioinfo.cipf.es/>

Processing / Normalization: RNA-Seq  
Expression / Differential Expression: RNA-Seq

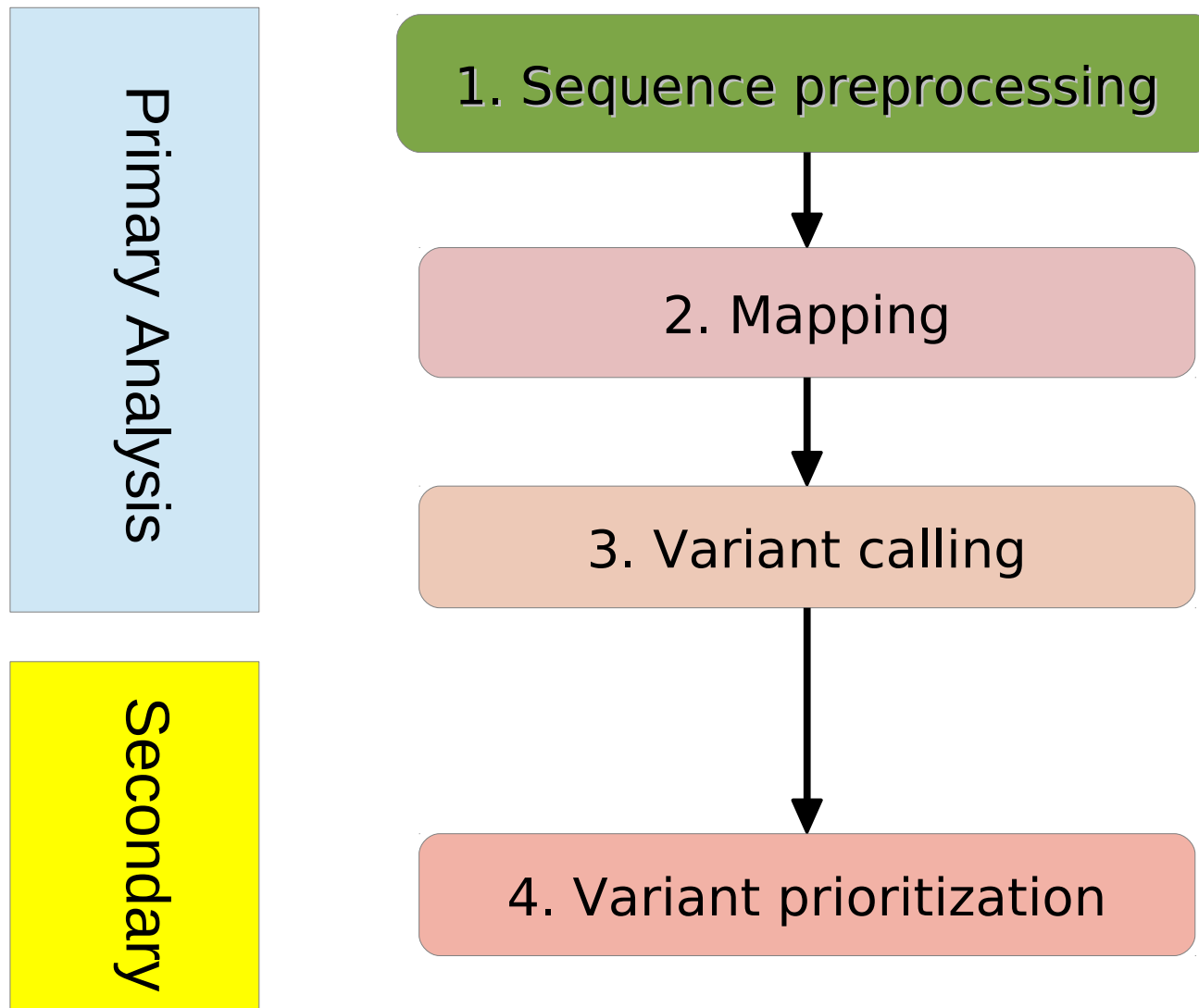
### Online examples

# Outline

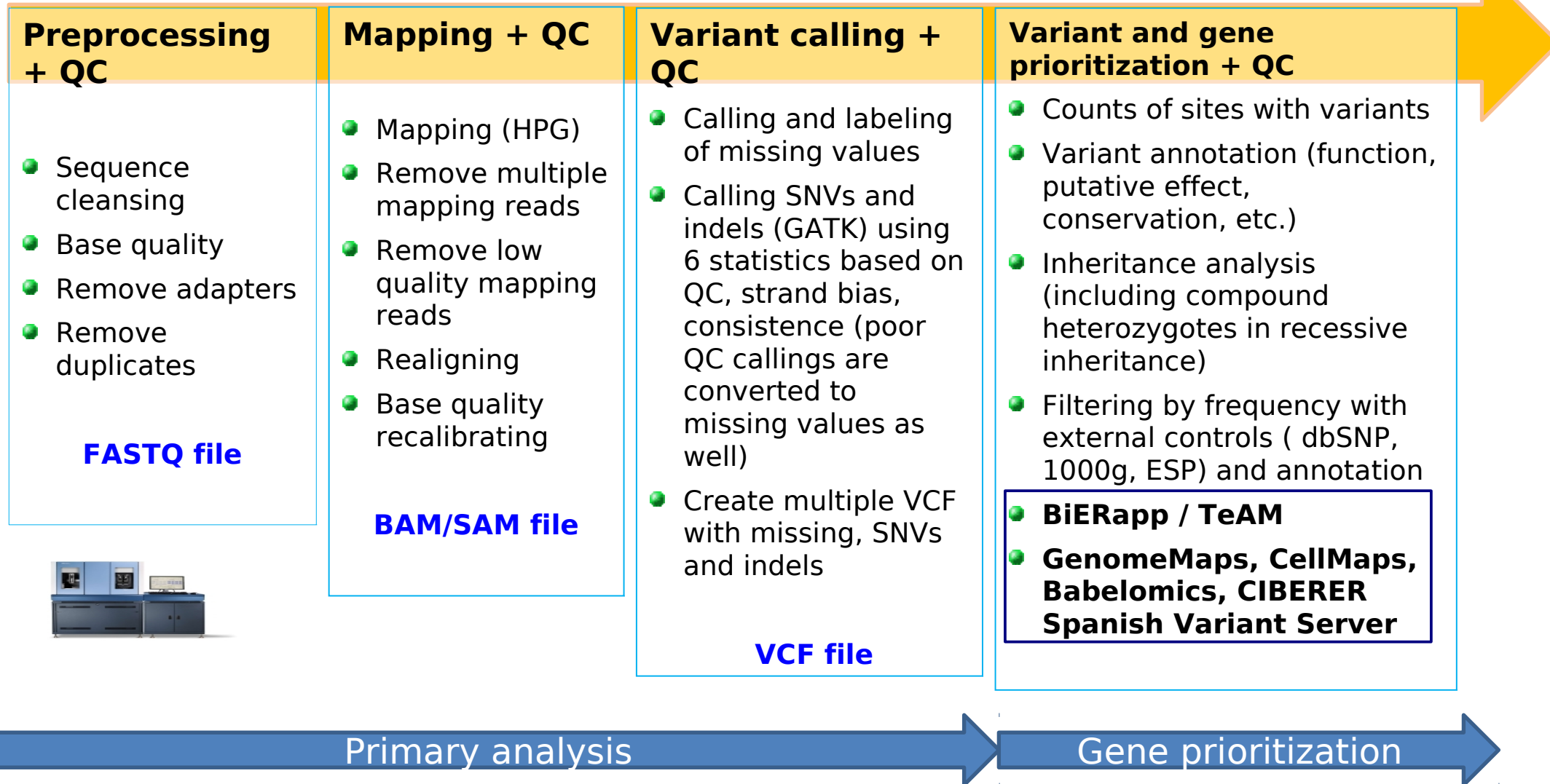
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- 1) Introduction to NGS Data Analysis
- 2) RNA-Seq Data Analysis
- 3) Resequencing Data Analysis**
  - 1) Pipeline Data Analysis
  - 2) BiERapp (Whole Exome Studies)
  - 3) TEAM (Gene Panel).
  - 4) CSVS (CIBERER Spanish Variant Server), Genome Maps, Cell Maps.
- 4) Omics Data Integration
- 5) Network Analysis

# Genomics Data Analysis Pipeline (1)



# Genomics Data Analysis Pipeline (2)





# BiERapp:

Una **herramienta web** para la  
priorización de variantes

<http://ciberer.es/bier/bierapp>

# Introduction

- Whole-exome sequencing has become a fundamental tool for the discovery of disease-related genes of familial diseases but there are difficulties to **find the causal mutation among the enormous background**
- There are different scenarios, so we need **different and immediate strategies of prioritization**
- Vast amount of **biological knowledge available** in many databases
- We need a tool to **integrate this information and filter immediately** to select candidate variants related to the disease

# How does BiERapp work?

Filterings

VCF file  
multisample

BiERapp

VARIANT

CellBase

Variant Browser

⌕

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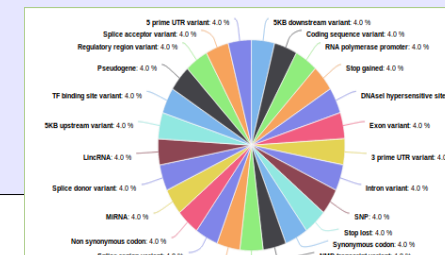
🔍

📄

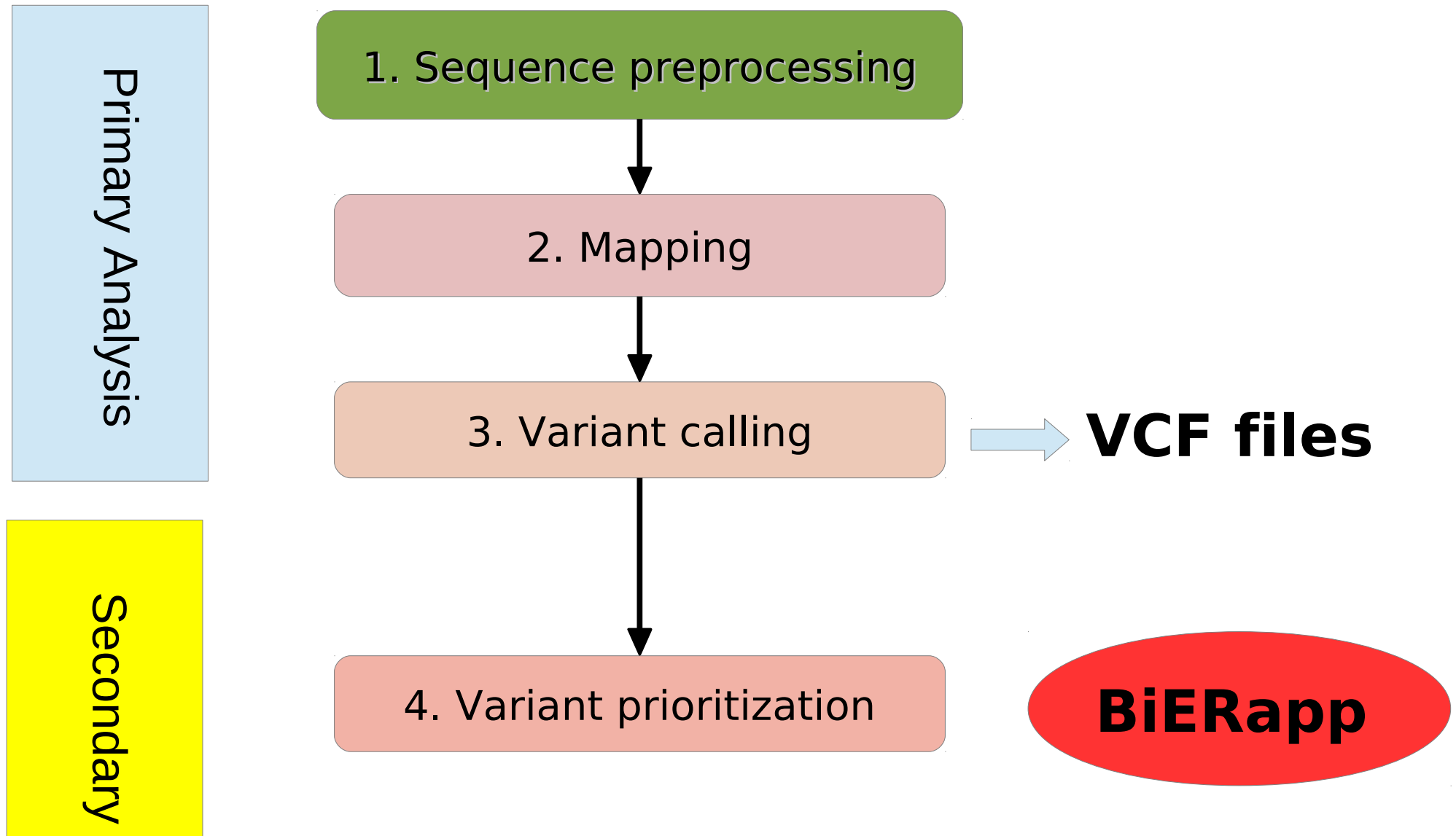
Variant: 1012211090

Variant	Allele	Gene	Samples				S.	Controls (NAF)						EVS	-	-	S.	P.
			NA19000	NA19060	NA19061	NA19065		1000G	1000G-ASR	1000G-ASR	1000G-AME	1000G-EUR						
4102514058	T-C	NFKB1	1/1	1/1	1/1	1/1	0.042 (T)	0.002 (T)	0.000 (T)	0.044 (T)	0.089 (T)	0.058	e.	.	.	.	.	
7123047703	T-C	CNDP4	1/1	1/1	1/1	1/1	0.023 (T)	0.025 (T)	0.000 (T)	0.025 (T)	0.000 (T)	0.012	e.	.	.	.	.	
579861270	T-C	HEXB	1/1	1/1	1/1	1/1	0.021 (T)	0.002 (T)	0.000 (T)	0.019 (T)	0.049 (T)	0.031	e.	.	.	.	.	
5109795608	T-C	CELSR2	1/1	1/1	1/1	1/1	0.070 (T)	0.228 (T)	0.004 (T)	0.036 (T)	0.036 (T)	0.086	e.	.	.	.	.	
1770943090	T-C	SLC39A11	1/1	1/1	1/1	1/1	0.087 (T)	0.344 (T)	0.002 (T)	0.055 (T)	0.001 (T)	0.106	e.	.	.	.	.	
1958879979	C-T	ZNF837	1/1	1/1	1/1	1/1	0.094 (C)	0.132 (C)	0.079 (C)	0.083 (C)	0.073 (C)	0.066	e.	.	.	.	.	
1778289638	A-G	RNF213	1/1	1/1	1/1	1/1	0.000 (A)	0.000 (A)	0.000 (A)	0.000 (A)	0.000 (A)	.	e.	.	.	.	.	
8145795382	T-C	LINC4	1/1	1/1	1/1	1/1	0.068 (T)	0.010 (T)	0.233 (T)	0.089 (T)	0.003 (T)	0.001	S.	.	.	.	.	
1012211090	T-C	DHTRD1	1/1	1/1	1/1	0/1	0.019 (T)	0.077 (T)	0.000 (T)	0.008 (T)	0.000 (T)	0.023	e.	.	.	.	.	
1210572982	A-G	KIRC3	1/1	1/1	1/1	1/1	0.011 (A)	0.043 (A)	0.000 (A)	0.035 (A)	0.000 (A)	0.035	e.	.	.	.	.	

Variant Data



# Input: VCF file



# Input: VCF multisample

```
##fileformat=VCFv4.1
##fileDate=20090805
##source=myImputationProgramV3.1
##reference=file:///seq/references/1000GenomesPilot-NCBI36.fasta
##contig=<ID=20,length=62435964,assembly=B36,md5=f126cdf8a6e0c7f379d618ff66beb2da,species="Homo sapiens",taxonomy=x>
##phasing=partial
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##INFO=<ID=AF,Number=A,Type=Float,Description="Allele Frequency">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP membership, build 129">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FILTER=<ID=q10,Description="Quality below 10">
##FILTER=<ID=s50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT NA00001 NA00002 NA00003
20 14370 rs6054257 G A 29 PASS NS=3;DP=14;AF=0.5;DB;H2 GT:GQ:DP:HQ 0|0:48:1:51,51 1|0:48:8:51,51 1/1:43:5:..
20 17330 . T A 3 q10 NS=3;DP=11;AF=0.017 GT:GQ:DP:HQ 0|0:49:3:58,50 0|1:3:5:65,3 0/0:41:3
20 1110696 rs6040355 A G,T 67 PASS NS=2;DP=10;AF=0.333,0.667;AA=T;DB GT:GQ:DP:HQ 1|2:21:6:23,27 2|1:2:0:18,2 2/2:35:4
20 1230237 . T . 47 PASS NS=3;DP=13;AA=T GT:GQ:DP:HQ 0|0:54:7:56,60 0|0:48:4:51,51 0/0:61:2
20 1234567 microsat1 GTC G,GTCT 50 PASS NS=3;DP=9;AA=G GT:GQ:DP 0/1:35:4 0/2:17:2 1/1:40:3
```

**One VCF (Variant Calling Format) file  
for family or group**

# Getting information

## □ SIFT

- SIFT predicts whether an amino acid substitution affects protein function
- **Interpretation:** 1 (tolerated) to 0 (not tolerated)

<http://sift.jcvi.org/>



## □ PolyPhen

- Polymorphism Phenotyping is a tool which predicts possible impact of an amino acid substitution on the structure and function of a human protein
- **Interpretation:** 1 (probably damage) to 0 (benign)

<http://genetics.bwh.harvard.edu/pph2/index.shtml>



# Getting information

**e!Ensembl** BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation

Using this website | **Annotation & prediction** | Data access | API & software | About us

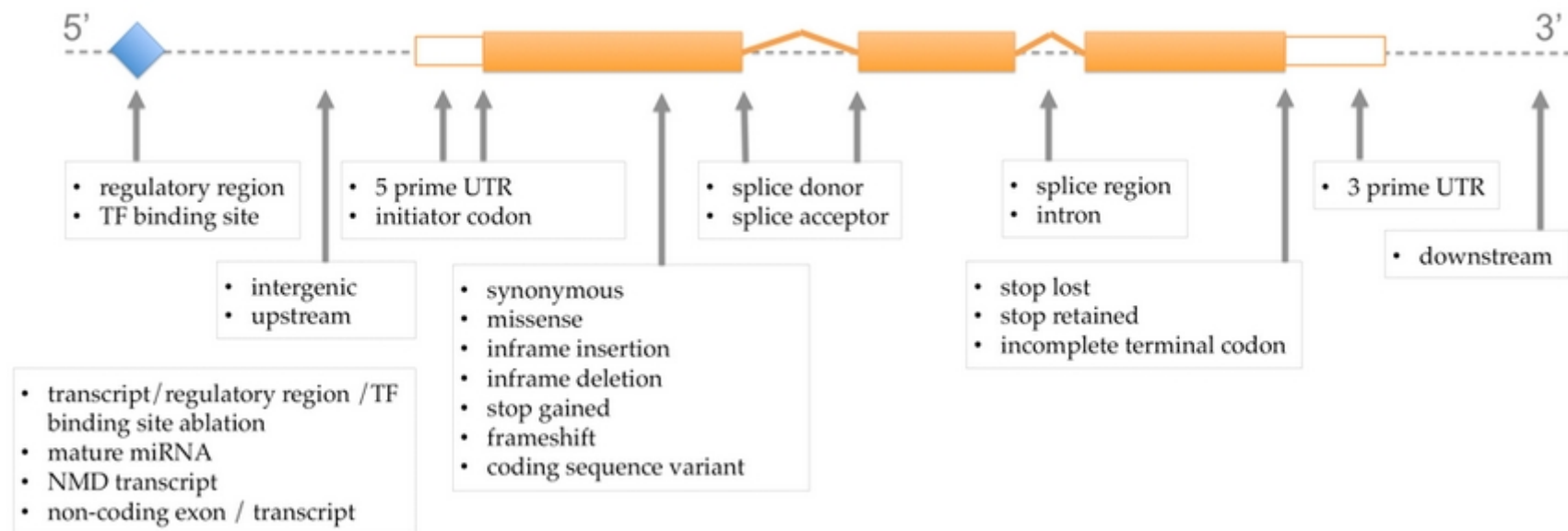
In this section

- Data Description
- Predicted Data
- Import VCF script
- Variation Sources

Home > Help & Documentation > Annotation & Prediction

## Ensembl Variation - Predicted data

## Consequence type or effect




[http://www.ensembl.org/info/genome/variation/predicted\\_data.html](http://www.ensembl.org/info/genome/variation/predicted_data.html)



# Tool interface

<http://ciberer.es/bier/bierapp>

[Menu](#) **BierApp**  [Home](#)

## Overview

Welcome to the gene/variant prioritization tool of the BIER (the Team of Bioinformatics for Rare Diseases). This interactive tool allows finding genes affected by deleterious variants that segregate along family pedigrees, case-controls or sporadic samples.







## Try an Example

Here you can try all the filtering options and discover the gene affected in a test family.

## Analyze your own families or case-control data

Here you can upload your VCF file containing the exomes to be analyzed. Define the thresholds of allele frequencies, pathogenicity, conservation; the type of variants sought; and define the type of inheritance and the segregation schema along the family.

Supported by



[logout](#) [upload & manage](#) [profile](#) [jobs](#) [support](#)

# Tool interface

Menu BierApp Home

Example 1000G (Short)

Filter

Clear Submit

Segregation

	0/0	0/1	1/1
NA19600:	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
NA19660:	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
NA19661:	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
NA19685:	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

MAF

1000G MAF <: 0.1

EVS MAF <:

1000G Populations

African MAF <:

American MAF <:

Asian MAF <:

European MAF <:

Position

Consequence Type

- ☐ SKB\_downstream\_variant
- ☐ coding\_sequence\_variant
- ☐ RNA\_polymerase\_promoter
- ☐ stop\_gained
- ☐ DNaseI\_hypersensitive\_site
- ☒ exon\_variant
- ☐ 3\_prime\_UTR\_variant
- ☐ intron\_variant
- ☐ SNP
- ☐ stop\_lost
- ☐ synonymous\_codon
- ☐ NMD\_transcript\_variant
- ☐ CpG\_island
- ☐ miRNA\_target\_site

Variant Browser

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Variant	Alleles	Gene	Samples				Controls (MAF)						Variants 1-10 of 85		
			NA19600	NA19660	NA19661	NA19685	1000G	1000G-AMR	1000G-ASI	1000G-AME	1000G-EUR	EVS	...	...	...
4:103514658	T>C	NFKB1	1/1	1/1	1/1	1/1	0.042(T)	0.002(T)	0.000(T)	0.064(T)	0.089(T)	0.058	e...	.	.
7:135047703	T>C	CNOT4	1/1	1/1	1/1	1/1	0.013(T)	0.055(T)	0.000(T)	0.005(T)	0.000(T)	0.012	e...	.	.
5:73981270	T>C	HEXB	1/1	1/1	1/1	1/1	0.021(T)	0.002(T)	0.000(T)	0.019(T)	0.049(T)	0.031	e...	0...	0...
1:109795608	T>C	CELSR2	1/1	1/1	1/1	1/1	0.070(T)	0.228(T)	0.004(T)	0.036(T)	0.036(T)	0.086	e...	1...	.
17:70943990	T>C	SLC39A11	1/1	1/1	1/1	1/1	0.087(T)	0.344(T)	0.002(T)	0.055(T)	0.001(T)	0.106	e...	0...	0...
19:58879976	C>T	ZNF837	1/1	1/1	1/1	1/1	0.094(C)	0.152(C)	0.079(C)	0.083(C)	0.073(C)	0.066	e...	0...	0...
17:78298938	A>G	RNF213	1/1	1/1	1/1	1/1	0.000(A)	0.000(A)	0.000(A)	0.000(A)	0.000(A)	.	e...	0...	1...
8:145745182	T>C	LRRC14	1/1	1/1	1/1	1/1	0.068(T)	0.010(T)	0.203(T)	0.069(T)	0.003(T)	0.001	5...	0...	.
10:12111090	T>C	DHTRD1	1/1	1/0	1/1	0/1	0.019(T)	0.077(T)	0.000(T)	0.008(T)	0.000(T)	0.033	e...	0...	0...

Variant Data

Genomic Context Effect & Annotation Study Summary

Effects

Num variants: 1000

Num samples: 4

Num indels: 21

Num biallelic: 1000

Num multiallelic: 0

Num transitions: 748

Num transversions: 231

% PASS: 100%

Ti/Tv Ratio: 3.24

Avg. Quality: 106.90

Consequence type

5 prime UTR variant: 4.0 %

SKB downstream variant: 4.0 %

Coding sequence variant: 4.0 %

RNA polymerase promoter: 4.0 %

Stop gained: 4.0 %

DNaseI hypersensitive site: 4.0 %

Exon variant: 4.0 %

3 prime UTR variant: 4.0 %

Intron variant: 4.0 %

SNP: 4.0 %

Stop lost: 4.0 %

Synonymous codon: 4.0 %

NMD transcript variant: 4.0 %

CpG island: 4.0 %

MIRNA target site: 4.0 %

Non synonymous codon: 4.0 %

Splice donor variant: 4.0 %

LincRNA: 4.0 %

SKB upstream variant: 4.0 %

TF binding site variant: 4.0 %

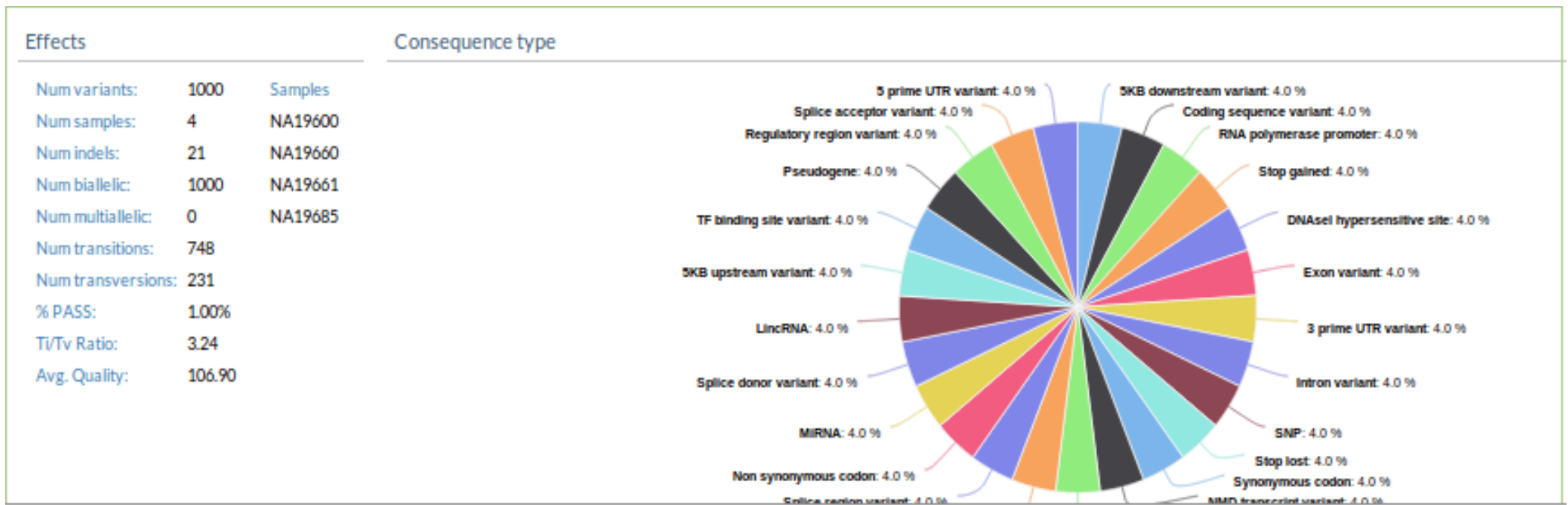
Pseudogene: 4.0 %

Regulatory region variant: 4.0 %

Splice acceptor variant: 4.0 %

# Results

**1. Summary.** Description about number of variants, INDELs... Also a distribution of consequences types.



# Results

## 2. List of candidate variants.

We can order this list by several criteria.

Variant Browser

« ‹ | Page 1 of 9 | › » | 🔍

Variants 1 - 10 of 85

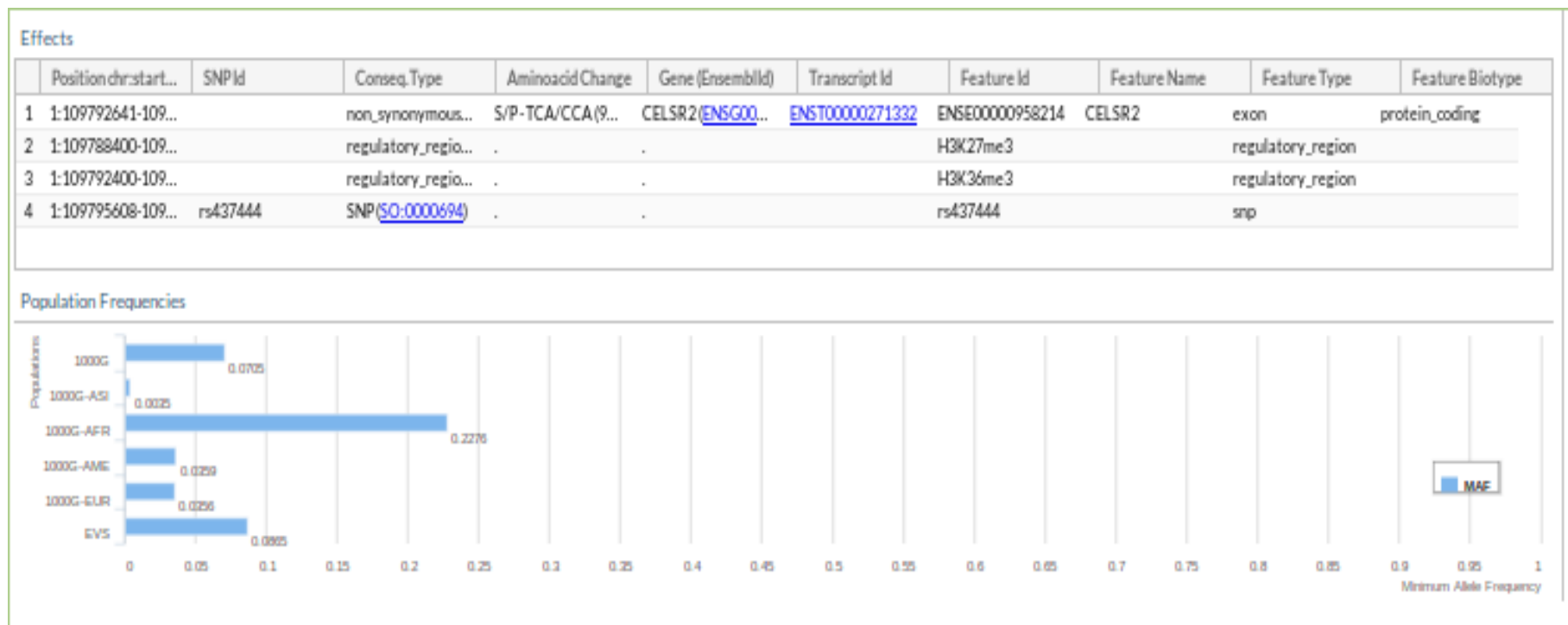
Variant	Alleles	Gene	Samples				S..	Controls (MAF)						...	...	S..	Ph
			NA19600	NA19660	NA19661	NA19685		1000G	1000G-AFR	1000G-ASI	1000G-AME	1000G-EUR	EVS				
4:103514658	T>C	NFKB1	1/1	1/1	1/1	1/1		0.042 (T)	0.002 (T)	0.000 (T)	0.064 (T)	0.089 (T)	0.058	e..	.	.	
7:135047703	T>C	CNOT4	1/1	1/1	1/1	1/1		0.013 (T)	0.055 (T)	0.000 (T)	0.005 (T)	0.000 (T)	0.012	e..	.	.	
5:73981270	T>C	HEXB	1/1	1/1	1/1	1/1		0.021 (T)	0.002 (T)	0.000 (T)	0.019 (T)	0.049 (T)	0.031	e..	Q..	Q..	
1:109795608	T>C	CELSR2	1/1	1/1	1/1	1/1		0.070 (T)	0.228 (T)	0.004 (T)	0.036 (T)	0.036 (T)	0.086	e..	1..	.	
17:70943990	T>C	SLC39A11	1/1	1/1	1/1	1/1		0.087 (T)	0.344 (T)	0.002 (T)	0.055 (T)	0.001 (T)	0.106	e..	Q..	Q..	
19:58879976	C>T	ZNF837	1/1	1/1	1/1	1/1		0.094 (C)	0.152 (C)	0.079 (C)	0.083 (C)	0.073 (C)	0.066	e..	Q..	Q..	
17:78298938	A>G	RNF213	1/1	1/1	1/1	1/1		0.000 (A)	0.000 (A)	0.000 (A)	0.000 (A)	0.000 (A)	.	e..	Q..	1..	
8:145745182	T>C	LRRC14	1/1	1/1	1/1	1/1		0.068 (T)	0.010 (T)	0.203 (T)	0.069 (T)	0.003 (T)	0.001	5..	Q..	.	
10:12111090	T>C	DHTKD1	1/1	1/0	1/1	0/1		0.019 (T)	0.077 (T)	0.000 (T)	0.008 (T)	0.000 (T)	0.033	e..	Q..	Q..	
12:10572982	A>G	KLRC3	1/1	1/1	1/1	1/1		0.011 (A)	0.043 (A)	0.000 (A)	0.005 (A)	0.000 (A)	0.015	e..	.	.	

Variant Data

# Results

## 3. Effects for each transcript where we detected a candidate variant.

The plot shows MAFs for different groups (1000 Genomes, Exome Variant Server)



# Results

## 4. Visualization of candidate variants from GenomeMaps

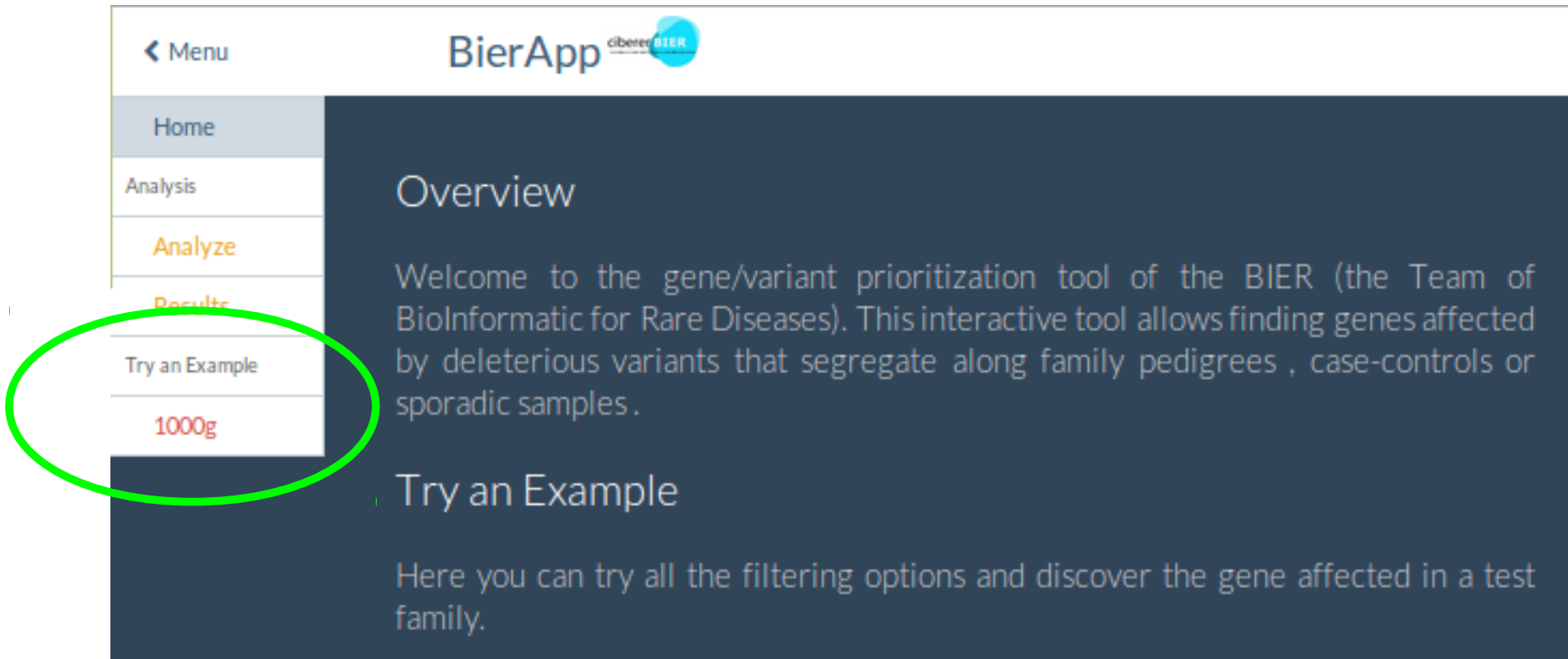


# Remarks

- The proposed web-based interactive framework has **great potential to detect disease-related variants** in familial diseases as demonstrated by its successful use in several studies
- **The use of the filters is interactive** and the results are almost instantaneously displayed in a panel that includes the genes affected, the variants and specific information for them
- Candidate variants are **new knowledge useful for future diagnostic**

# Hands on

<http://bioinfo.cipf.es/apps-beta/cibererapp/beta/>



**BierApp** ciberer BIER

Menu

- Home
- Analysis
- Analyze
- Results
- Try an Example**
- 1000g

## Overview

Welcome to the gene/variant prioritization tool of the BIER (the Team of BioInformatic for Rare Diseases). This interactive tool allows finding genes affected by deleterious variants that segregate along family pedigrees, case-controls or sporadic samples.

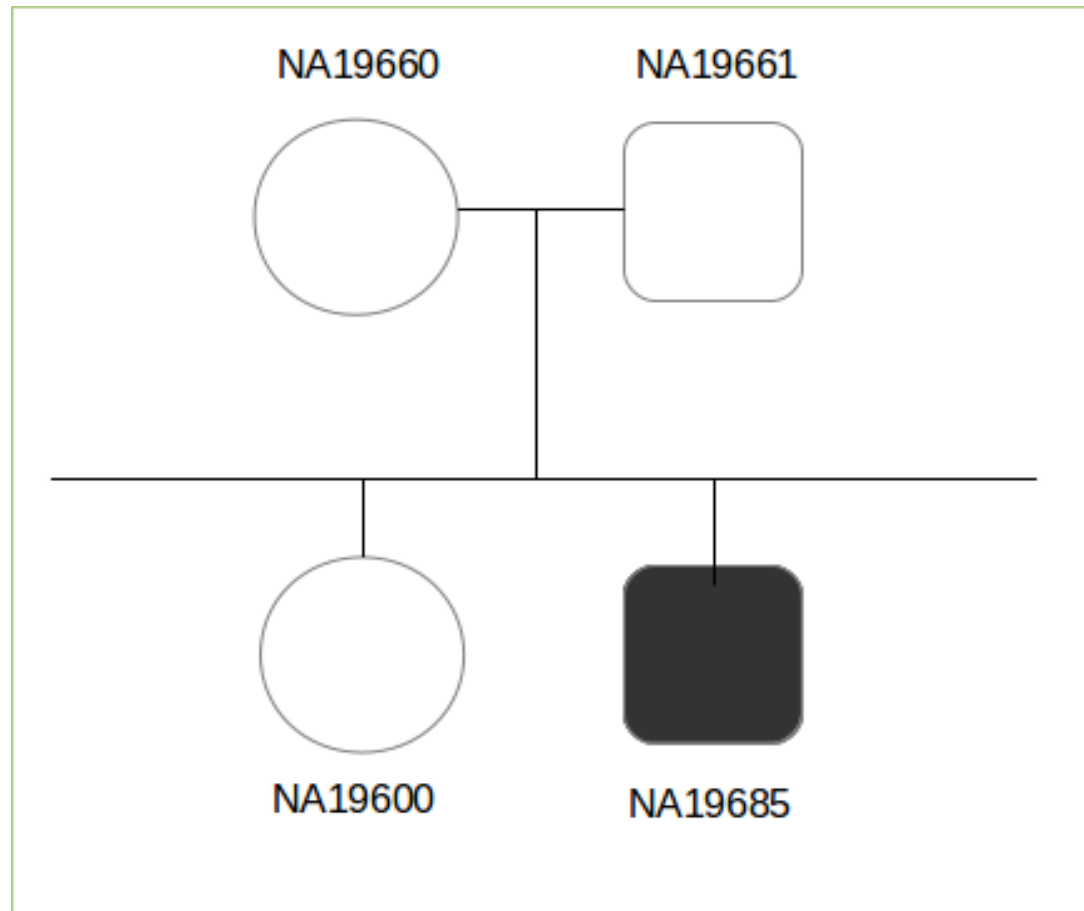
## Try an Example

Here you can try all the filtering options and discover the gene affected in a test family.



# Hands on

## Pedigree



# Hands on

## Case 1.

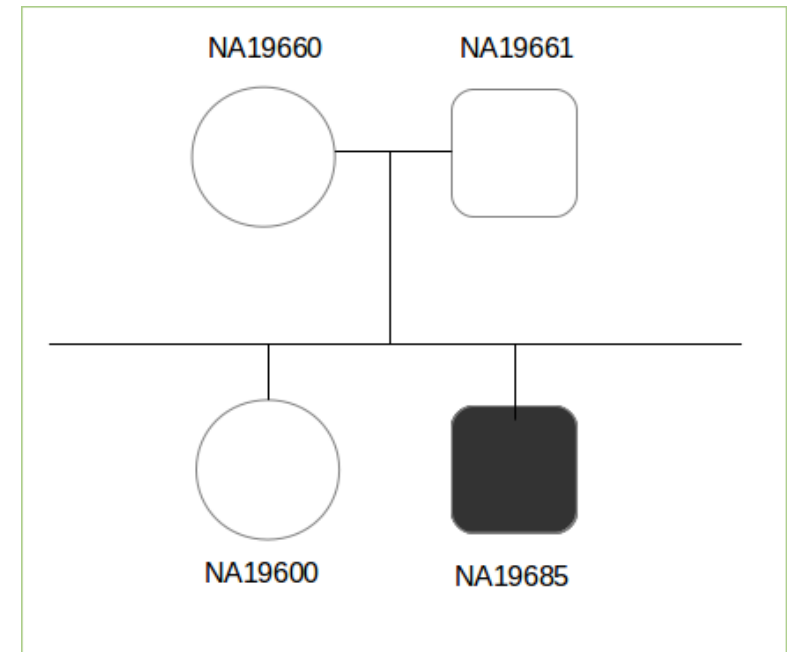
- Dominant heritage

How many variants? **14**

## Case 2.

- Recessive heritage

How many variants? **3**

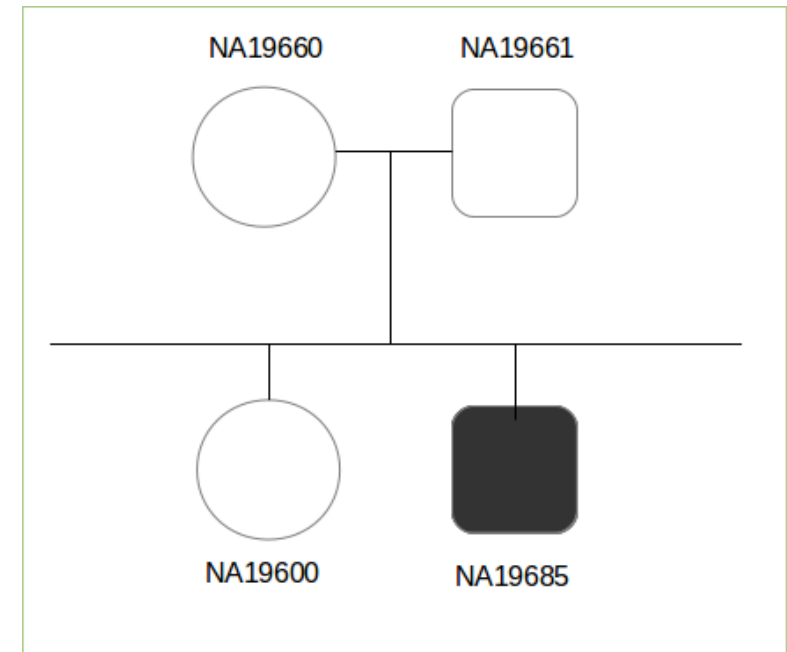


# Hands on

## Case 3.

- Dominant heritage
- Rare disease (MAF < 0.1)

How many variants? **7**



## Case 4.

- Variants in mother and daughter at the same time

How many variants? **85**

# Hands on

## Case 5.

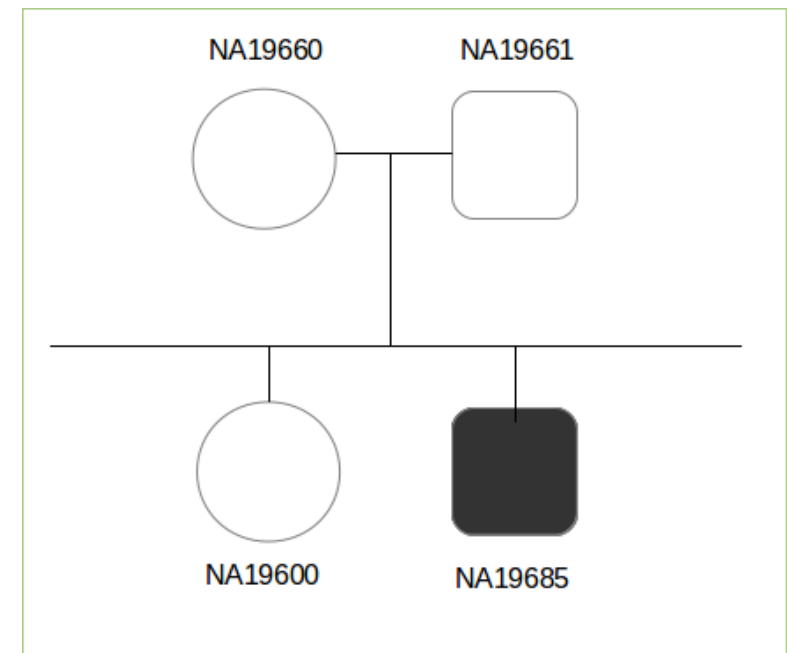
- Variants in mother and daughter at the same time
- Only in chromosome 4

How many variants?

## Case 6.

- Variants in mother and daughter at the same time
- Only in these genes: HEXB, NFKB1, KLRC3

How many variants?



# TEAM:

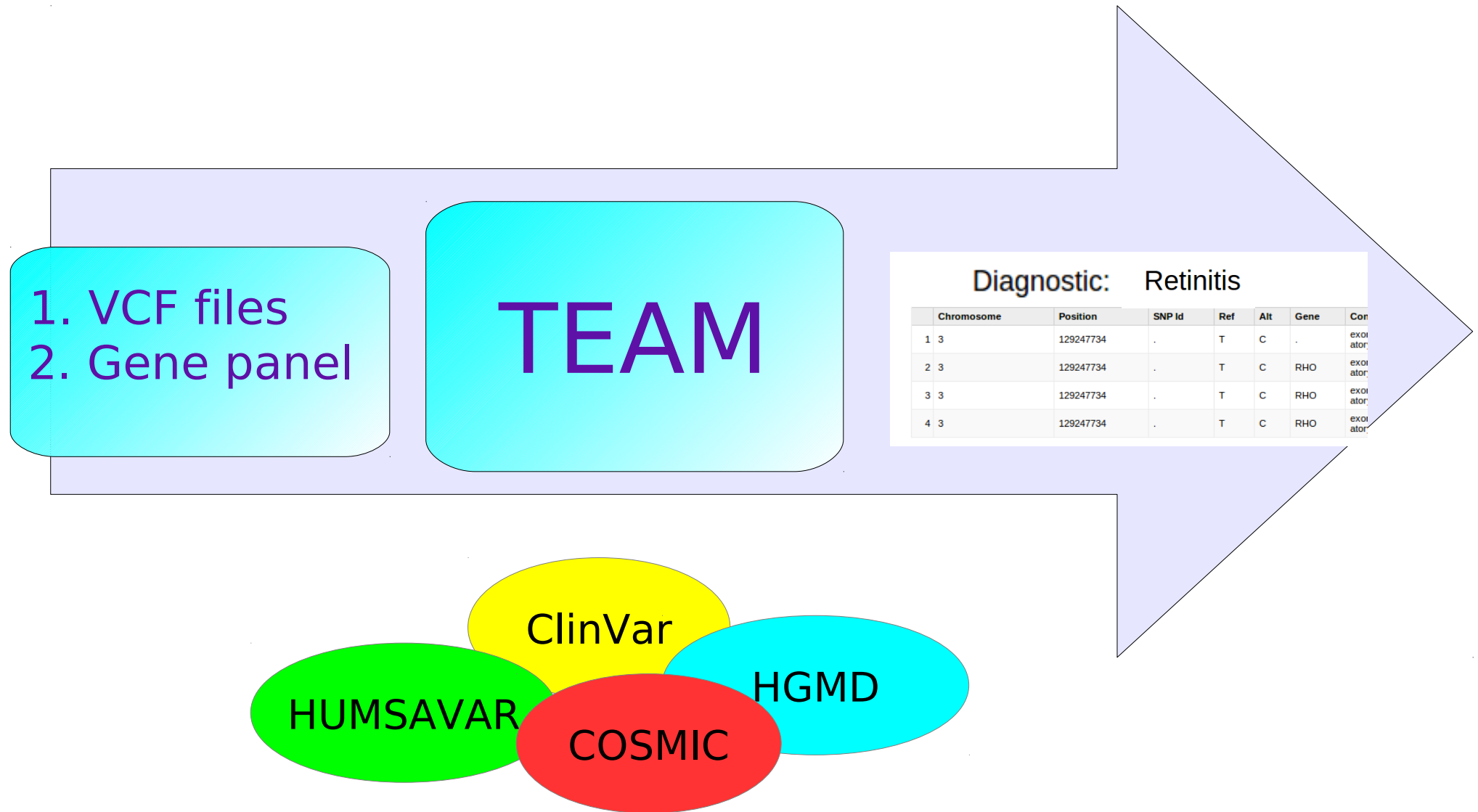
Una **herramienta web** para el diseño y gestión de **paneles de genes** en secuenciación dirigida con aplicaciones clínicas

[\*\*http://ciberer.es/bier/team\*\*](http://ciberer.es/bier/team)

# Introduction

- **Development of high throughput sequencing technologies:**
  - Rapid and economical genome sequencing.
  - Disease targeted sequencing: powerful and cost-effective application.
- **Vast amount of biological knowledge available:**
  - HGMD-public, HUMSAVAR, ClinVar, COSMIC.
- We need a tool to connect **sequencing data and biological knowledge for diagnostic:**
  - **TEAM** (Targeted Enrichment Analysis and Management).

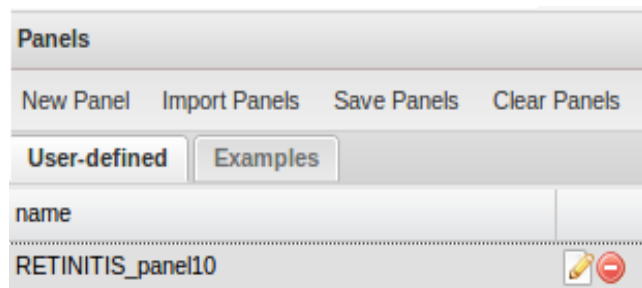
# How does TEAM work?



# How does TEAM work?

<http://ciberer.es/bier/team>

## 1. Defining panel



Panels

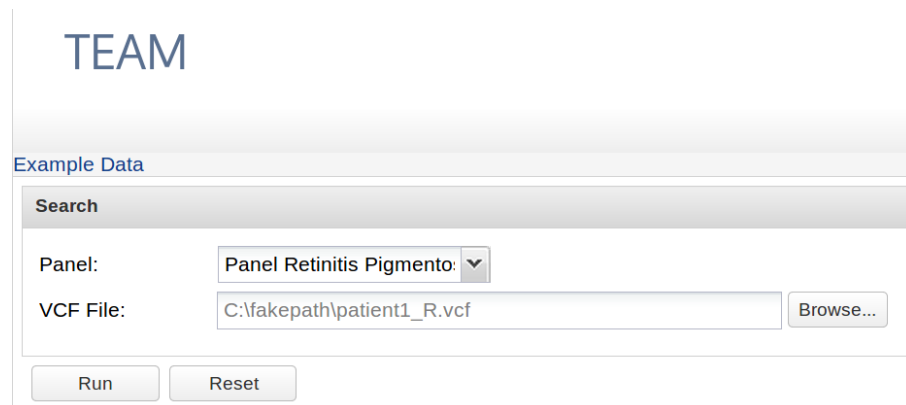
New Panel Import Panels Save Panels Clear Panels

User-defined Examples

name

RETINITIS\_panel10

## 2. Uploading input data



TEAM

Example Data

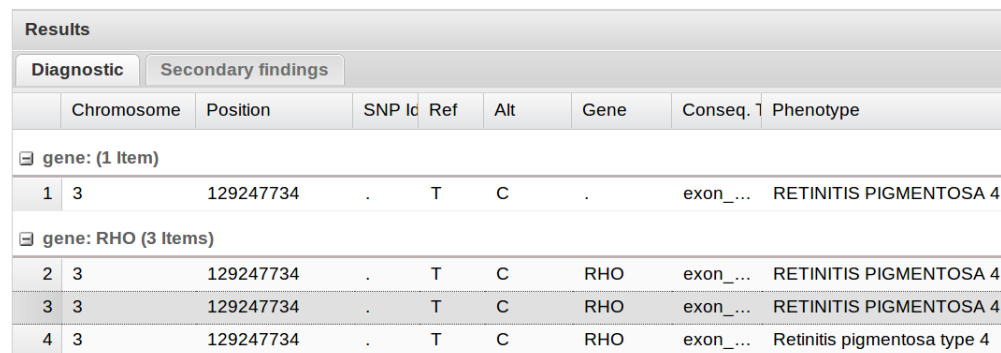
Search

Panel: Panel Retinitis Pigmento

VCF File: C:\fakepath\patient1\_R.vcf Browse...

Run Reset

## 3. Getting results



Results							
Diagnostic Secondary findings							
	Chromosome	Position	SNP Id	Ref	Alt	Gene	Conseq. 1 Phenotype
gene: (1 Item)							
1	3	129247734	.	T	C	.	exon_... RETINITIS PIGMENTOSA 4
gene: RHO (3 Items)							
2	3	129247734	.	T	C	RHO	exon_... RETINITIS PIGMENTOSA 4
3	3	129247734	.	T	C	RHO	exon_... RETINITIS PIGMENTOSA 4
4	3	129247734	.	T	C	RHO	exon_... Retinitis pigmentosa type 4



# How to define a panel?

1. Name of panel

2. Diseases

3. Adding:  
- more genes  
- mutations

4. Save panel

The screenshot shows the 'Panel Manager' window. A blue arrow points to the 'Name:' field, which contains 'RETINITIS\_10'. Another blue arrow points to the 'Diseases (Drag)' list, specifically to 'RETINITIS PIGMENTOSA 14'. A third blue arrow points to the 'Add Mutation' button. A fourth blue arrow points to the 'Add Genes' button. A fifth blue arrow points to the 'Text' radio button and the 'BRCA2,PPL' text input field. The 'Genes' list on the right contains 'IMPDH1', 'PRPF8', and 'RPE65', each with a red minus button. The 'Mutations' table has columns for 'Chr', 'Pos', 'Ref', 'Alt', and 'Gene'. At the bottom, there are buttons for 'Add new panel', 'Clear', and 'Close'.

Panel Manager

Name: RETINITIS\_10

Diseases (Drag)

Name
Ataxia_and_retinitis_pigmentosa_with_isolate...
Hypoprebetalipoproteinemia,_acanthocytosis,...
Juvenile_retinitis_pigmentosa,_AIPL1-related
Neuropathy_ataxia_retinitis_pigmentosa_syn...
POSTERIOR COLUMN ATAXIA WITH RETINI...
Polyneuropathy, hearing loss, ataxia, retinitis ...
RETINITIS PIGMENTOSA 1
RETINITIS PIGMENTOSA 11
RETINITIS PIGMENTOSA 12
RETINITIS PIGMENTOSA 14
RETINITIS PIGMENTOSA 17
RETINITIS PIGMENTOSA 18
RETINITIS PIGMENTOSA 19
RETINITIS PIGMENTOSA 2
RETINITIS PIGMENTOSA 25
RETINITIS PIGMENTOSA 26
RETINITIS PIGMENTOSA 27

Primary Disease (Drop)

RETINITIS PIGMENTOSA 10
RETINITIS PIGMENTOSA 13
RETINITIS PIGMENTOSA 20

Genes

IMPDH1	-
PRPF8	-
RPE65	-

Mutations

Chr	Pos	Ref	Alt	Gene
-----	-----	-----	-----	------

RETINITIS

PolyPhen:

Sift:

Add Mutation

Add Genes

Text ☒ Bed File ☐

BRCA2,PPL

Add new panel Clear Close

# How to define a panel?

Add mutation

Chr: 8 Pos: 55539395 Ref: A Alt: T Gene Name: RP1 Disease Name: Lung cancer 2

Reset Check Add Mutation

Region overview Window size: 583 nts

55,539,104 55,539,395 55,539,686

Sequence: AAGCACATAACTAAAATTGCCGTTTGACAGGAGATAATCTATGTAAGAGGGAGATAAGTCTTTT

Gene

SNP P\_ESP\_8\_55539357 rs58051614 rs200135800 COSM486527  
8\_55539353 rs202016292 rs201613551 rs2293869 rs202057087  
rs202226256

T 8:55,539,394 Genome Viewer

Adding  
new mutations

Checking  
mutations from  
Genome Viewer

# Results

Results								
Diagnostic		Secondary findings						
	Chromosome	Position	SNP Id	Ref	Alt	Gene	Conseq. Type	Phenotype
gene: (1 item)								
1	3	129247734	.	T	C	.	exon_vari...	RETINITIS PIGMENTOSA 4
gene: RHO (3 items)								
2	Variant Effect - 3:129247734 T>C							
3		Position chr:start:end (strand)	SNP Id	Conseq. Type		Aminoacid Change		
4	1	3:129247734-129247734 (+)	CM920608	SNP (SO:0000694)		.		
	2	3:129247483-129247937 (+)		synonymous_codon (SO:00...		P/P - CCC/CCC (53)		
	3	3:129245550-129248350		regulatory_region_variant (...)		.		
	4	3:129247734-129247734 (+)	rs28933395	SNP (SO:0000694)		.		

A. Web results

B. PDF report

Diagnostic: Retinitis

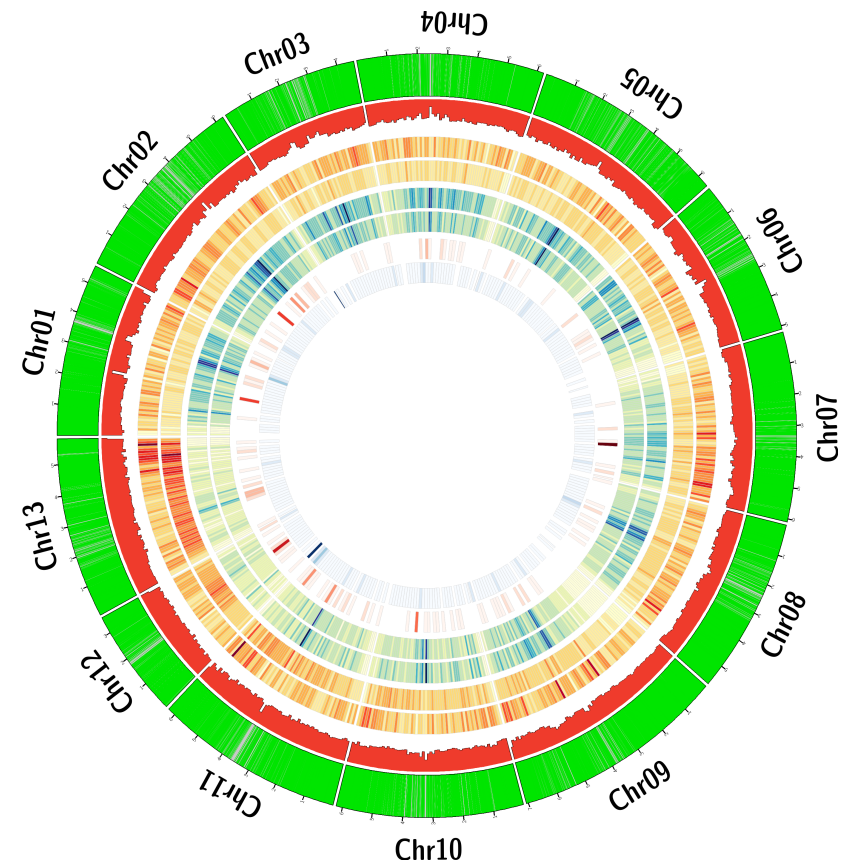
	Chromosome	Position	SNP Id	Ref	Alt	Gene	Con
1	3	129247734	.	T	C	.	exon
2	3	129247734	.	T	C	RHO	exon
3	3	129247734	.	T	C	RHO	exon
4	3	129247734	.	T	C	RHO	exon

# Remarks

- TEAM is an **free and easy-to-use web tool** that fills the gap between the enormous amounts of data in targeted enrichment sequencing analysis and the **biological knowledge** available.
- TEAM **provides an intuitive environment for the clinician** in which unprocessed data on patient's genomic variation can easily be transformed in a **diagnostic**.
- The entire patient's sequencing information is managed locally thus avoiding any problem of data **privacy or confidentiality**.

# Next improvements:

- Inclusion of a **database with public panels genes** of various diseases.
- **Comparative Analysis** for groups of panels.
- **Visualization results.**



# Hands on

[\*\*http://ciberer.es/bier/team\*\*](http://ciberer.es/bier/team)

- 1) Download **example data** from TEAM (3 VCF files).
- 2) **Select the panel** for Retinitis Pigmentosa and **evaluate all three samples**. Do you have variants related to Retinitis for each of the three patients?
- 3) **Generate a PDF report** for each patient including variants related to diagnostic and secondary findings.
- 4) **Design a new panel** for Usher disease.

# **CSVs:** **CIBERER Spanish Variant Server**

Repositorio de frecuencias de variantes  
en la población española

[\*\*http://csvs.babelomics.org/\*\*](http://csvs.babelomics.org/)

# Two initial repositories

- 1) <http://www.ciberer.es/bier/exome-server/>
- 2) <http://bioinfo.cipf.es/apps-beta/spv/1.0.1/>

# Spanish Population Variability

Filters

Reload

Clear

Search

Region/Gene

Region

Gene

Enter regions (comma separated)

2:1-1000000

Controls

Variant Info

Variant	Alleles	SNP Id	Gene	SPV				MAF
				Genotypes				
				0/0	0/1	1/1	./.	
2:14004	G>A			266	1	.	.	0.002
2:14190	C>T			266	1	.	.	0.002
2:14238	G>A			266	1	.	.	0.002
2:14296	G>A			266	1	.	.	0.002
2:14309	G>A			266	1	.	.	0.002
2:14485	T>C			240	27	.	.	0.051
2:14489	A>G			265	2	.	.	0.004
2:41366	C>T		FAM110C	259	6	2	.	0.019



# Tool interface

Spanish Population Variant Server **beta** Search Studies Stats ?

CLEAR SEARCH

Position

Chromosomal Location:

1:1-100000

Gene:

BRCA2, PPL

Search gene Q

Studies

- ☒ Mgp
- ☒ Virginia Nunes
- ☒ Miguel Angel Moreno
- ☒ Aurora Pujol
- ☒ Francesc Palau

Diseases

☐ Healthy Population

Chr	Position	Alleles	Id	MAF	1000G						EVS					
					Genotypes			Freq.			Genotypes			Freq.		
					0/0	0/1	1/1	0 freq	1 freq	MAF	0/0	0/1	1/1	0 freq	1 freq	MAF
1	17483	C>T		403	1	.	0.917	0.083	0.083							
1	18422	T>C		397	6	1	0.733	0.267	0.267							
1	18256	T>G		403	1	.	0.633	0.033	0.033							
1	18256	T>C		394	10	.	0.633	0.333	0.333							
1	18094	C>T		401	3	.	0.900	0.100	0.100							
1	17398	C>A		399	5	.	0.833	0.167	0.167							
1	16974	C>T		394	10	.	0.667	0.333	0.333							
1	16809	C>G		393	9	2	0.567	0.433	0.433							
1	16794	G>A		403	1	.	0.967	0.033	0.033							
1	16619	C>T		402	.	2	0.867	0.133	0.133							

Genomic Context Effect Frequencies Phenotype

Gene Name	Ensembl Gene Id	Ensembl Transcript Id	Conseq. type	Relative Position	Codon	Strand
Page 0 of 1						

Variants per Study

0k 200k 400k 600k 800k

Variants

<http://bioinfo.cipf.es/apps-beta/spvs/1.0.0/>

# Hands on

**<http://csvs.babelomics.org/>**

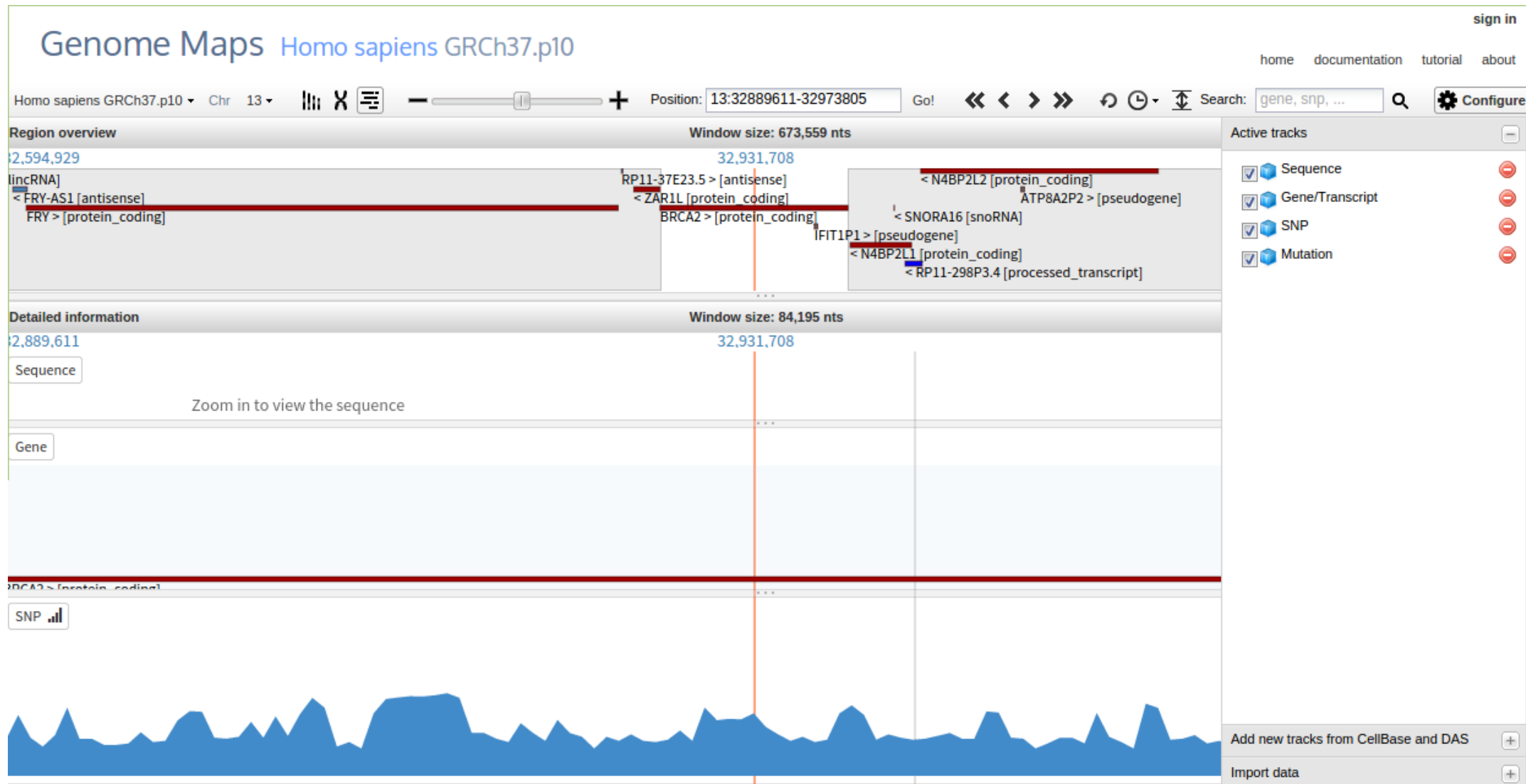
- 1) How many variants do you find in region: 1:24400-70000? (33 variants)
- 2) What information does CSPA give us for this position 1:24536? (Effect, phenotype...)

# Genome Maps

Visualizador genómico que interactúa  
con bases de datos funcionales

<http://genomemaps.org/>

# Tool interface



# Hands on

<http://genomemaps.org/>

- 1) Visualize this region: 1:100000-200000
- 2) Visualize this gene: LIN28A
- 3) Add new traks: miRNA, TFBS

# Cell Maps

Herramienta de modelización y  
visualización de redes biológicas

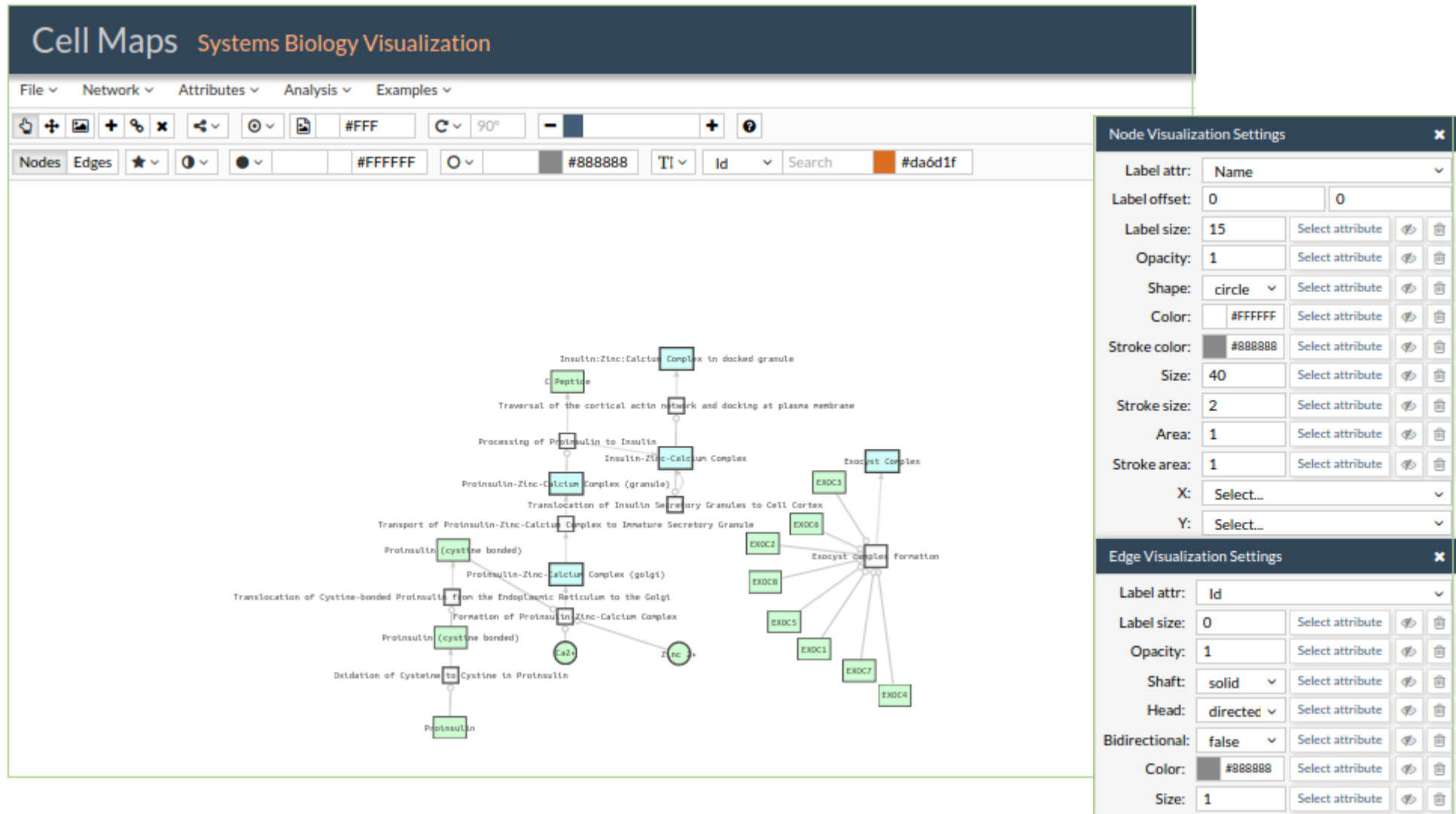
<http://cellmaps.babelomics.org/>

# Cell Maps

- 1) Es una herramienta que permite la integración, visualización y el análisis de redes biológicas.
- 2) El **input** es un fichero donde indicamos las relaciones entre los nodos de nuestra red. Opcionalmente podemos incluir un fichero con los atributos de cada nodo.
- 3) El **output gráfico** es una red en la que se muestran las relaciones de los distintos nodos que la integran.

**Tutorial:** <https://github.com/openCB/cell-maps/wiki>

# Tool interface



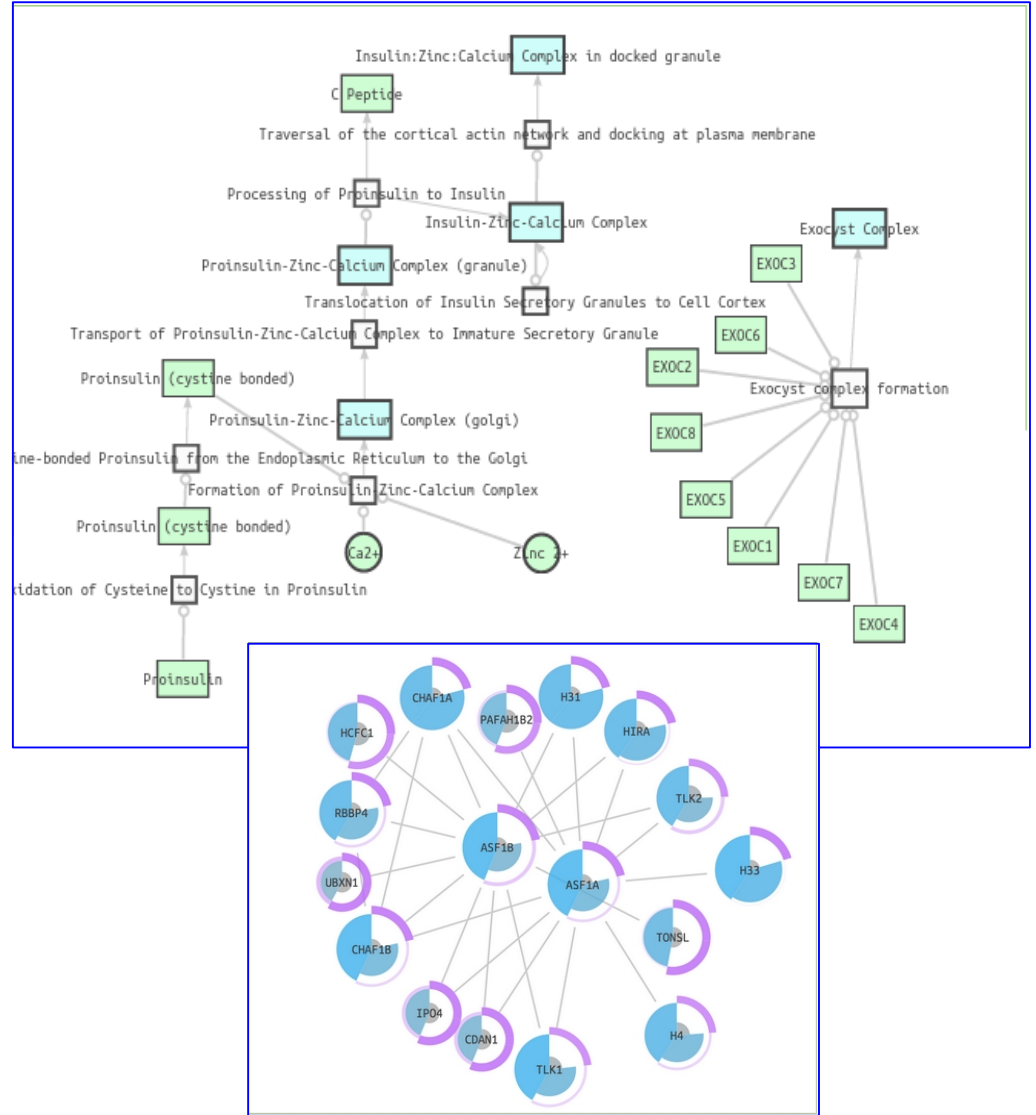
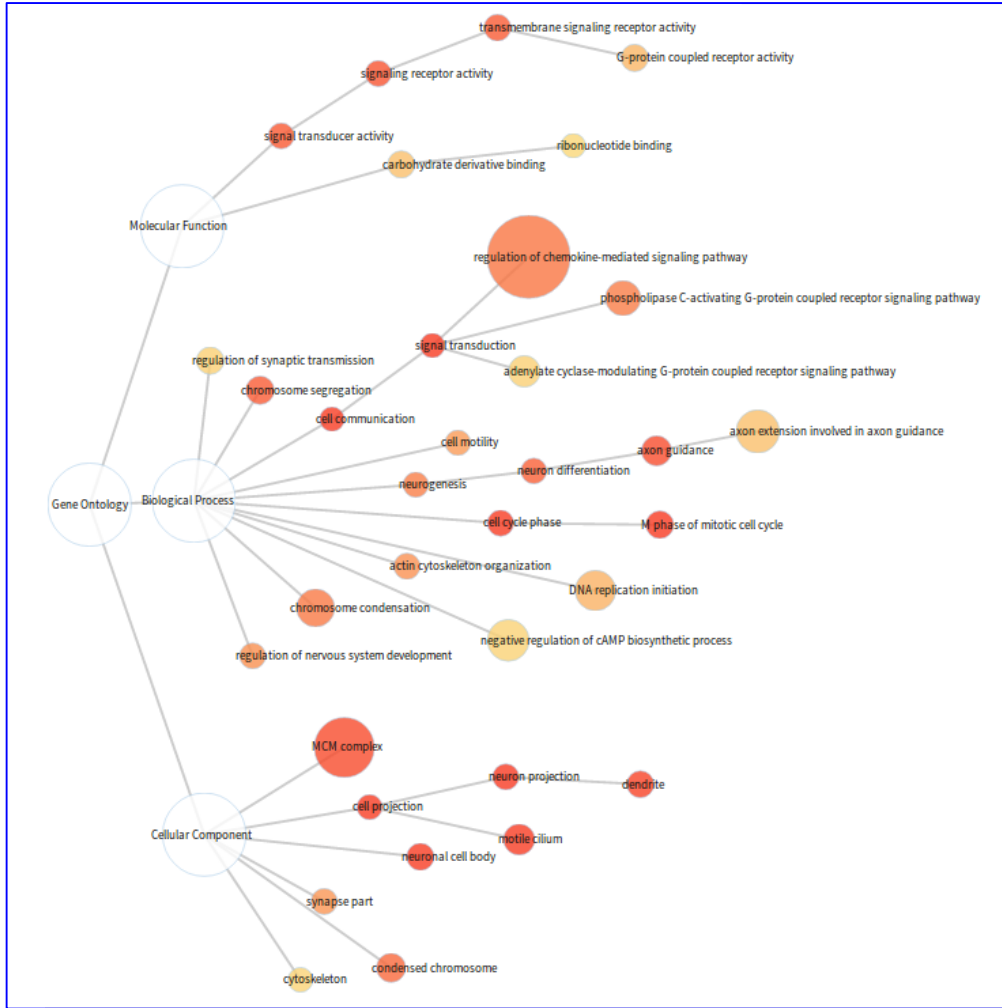


# Cell Maps: inputs

GO:0000001» pp» GO:0003674  
GO:0000001» pp» GO:0005575  
GO:0000001» pp» GO:0008150  
GO:0003674» pp» GO:0004871  
GO:0004871» pp» GO:0038023  
GO:0038023» pp» GO:0004888  
GO:0004888» pp» GO:0004930  
GO:0003674» pp» GO:0097367  
GO:0097367» pp»  
GO:0005575» pp»  
GO:0005575» pp»  
GO:0005575» pp»  
GO:0005575» pp»  
GO:0042995» pp»  
GO:0043005» pp»  
GO:0042995» pp»  
GO:0005575» pp»

ID	<u>pvalor</u>	indi2	descriptor
GO:0031514	0.001	0.16	motile cilium
GO:0000793	0.013	0.129	condensed chromosome
GO:0043025	0.001	0.1	neuronal cell body
GO:0030425	0.003	0.094	dendrite
GO:0044456	0.026	0.086	synapse part
GO:0043005	0.000	0.08	neuron projection
GO:0042995	0.001	0.067	cell projection
GO:0005856	0.044	0.059	<u>cytoskeleton</u>

# Cell Maps: outputs



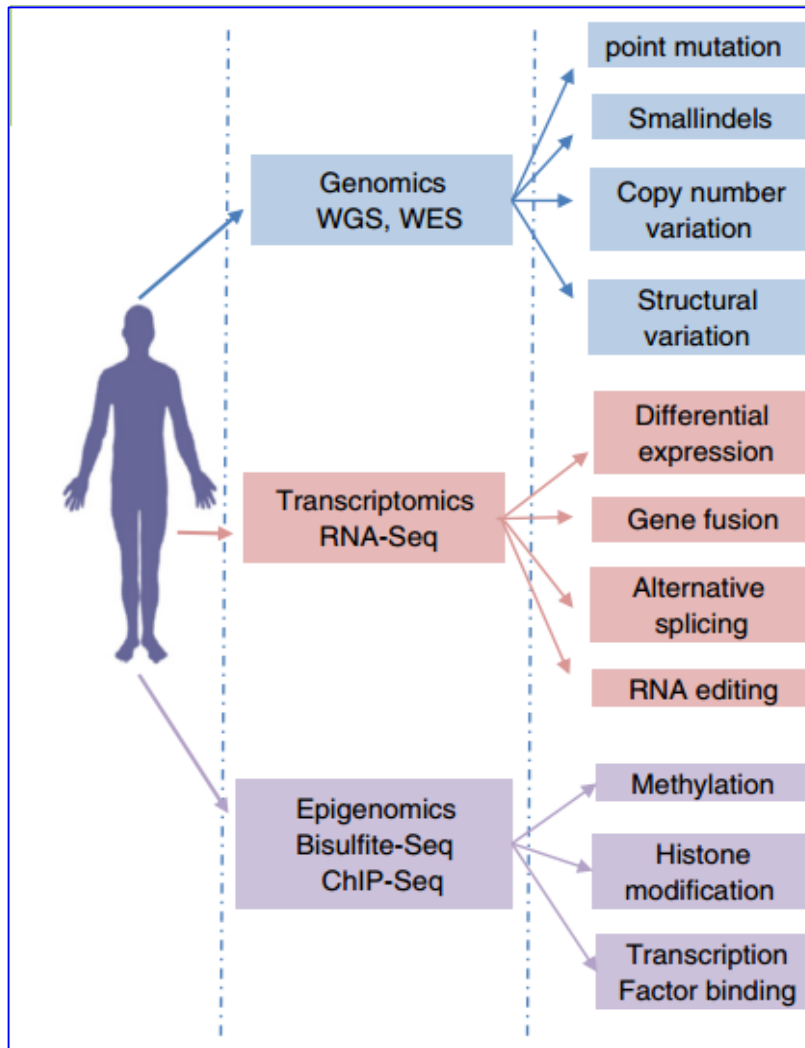
# Outline

---

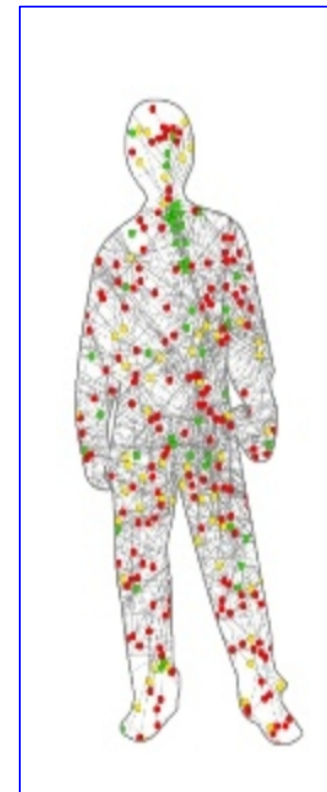
- 1) Introduction to NGS Data Analysis
- 2) RNA-Seq Data Analysis
- 3) Resequencing Data Analysis
- 4) **Omics Data Integration**
  - 1) Ad-hoc approaches
  - 2) Multidimensional Gene Set Analysis
  - 3) Functional Meta-Analysis
  - 4) PATHiVAR
- 5) Network Analysis

# Omic Data Integration

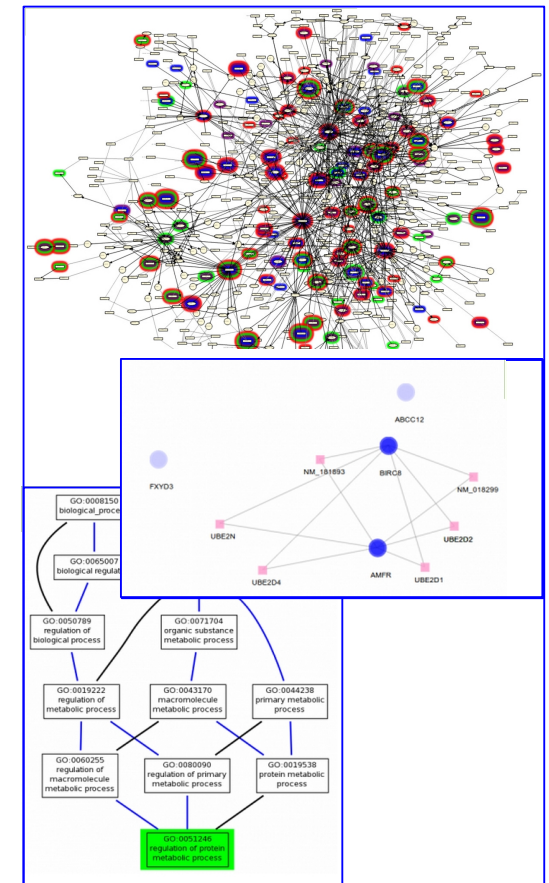
## Patient Technologies Data Analysis



## Integration and interpretation

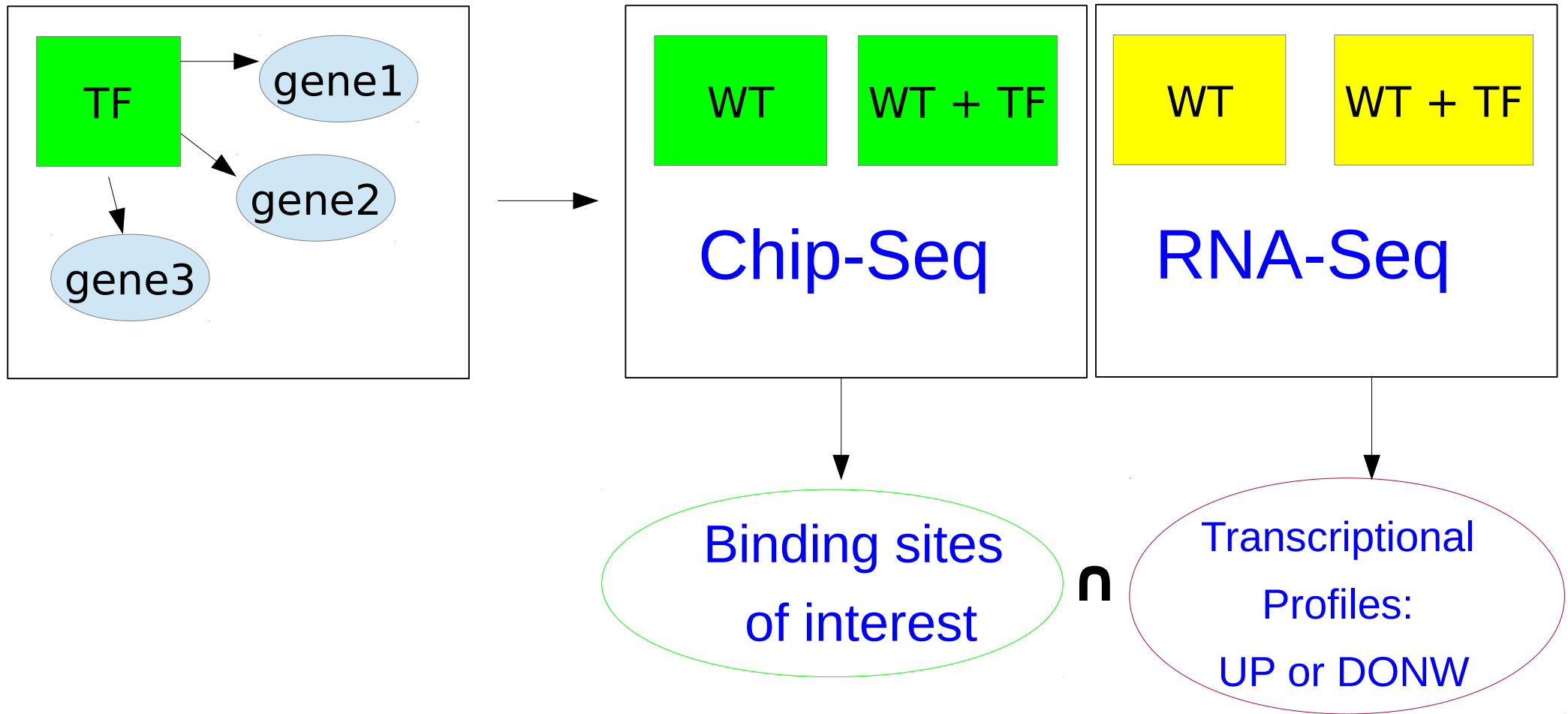


Molecular and clinical model



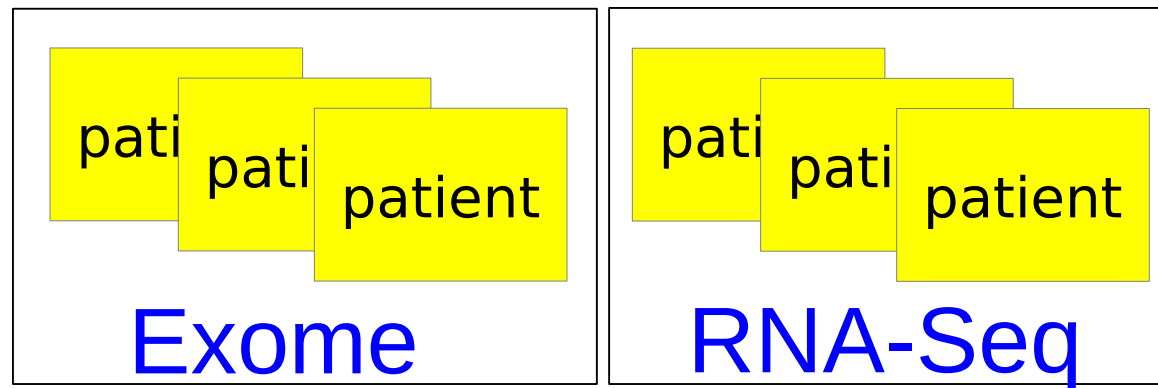
# Ad-hoc approaches (1)

## Chip-Seq & RNA-Seq



# Ad-hoc approaches (2)

## Exome & RNA-Seq

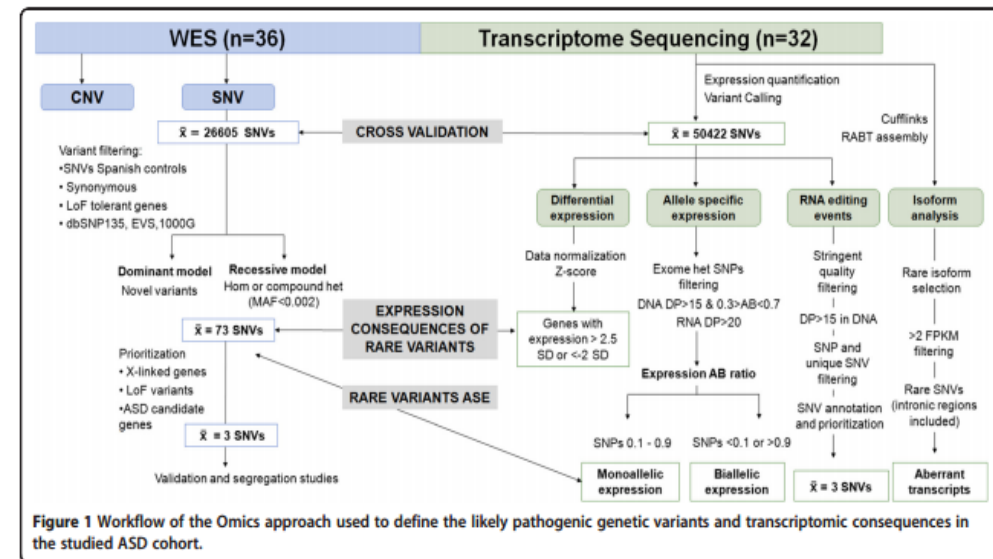


→ Intronic causative mutations

Exonic causative mutations

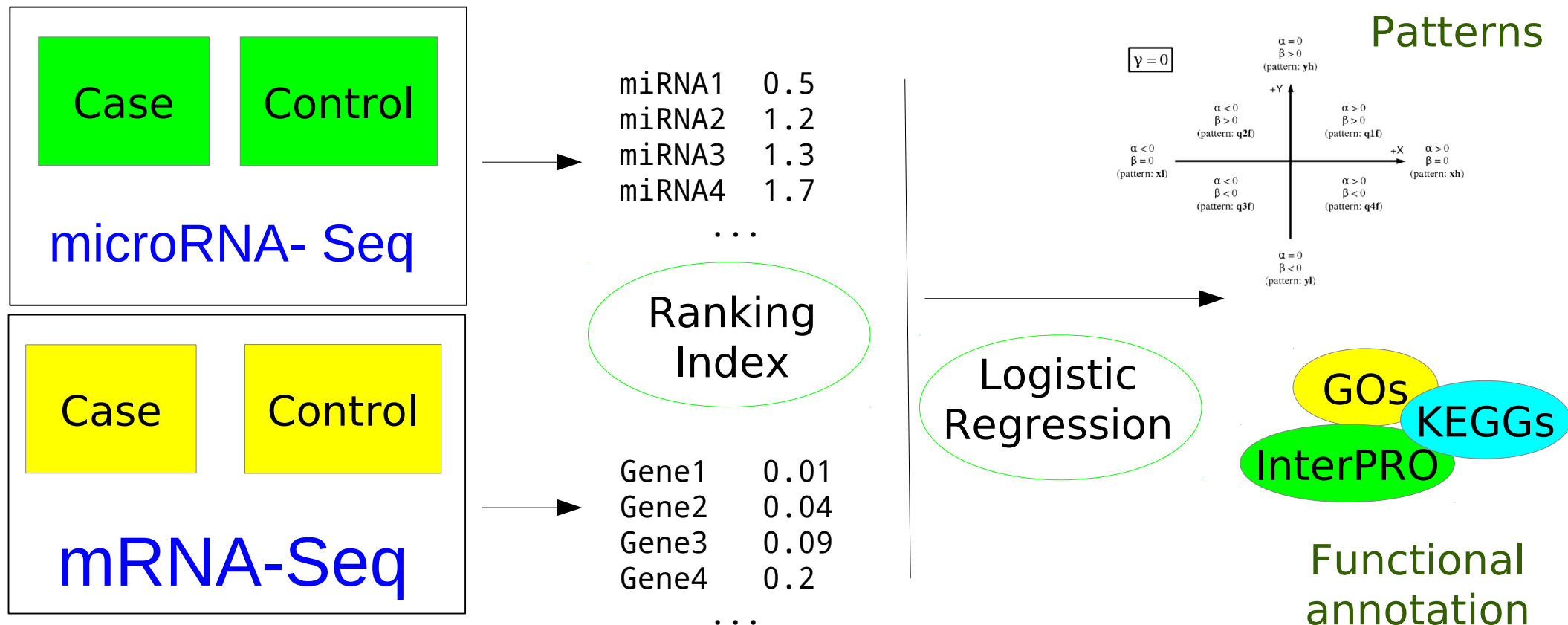
Integrated analysis of whole-exome sequencing and transcriptome profiling in males with autism spectrum disorders

Marta Codina-Solà<sup>1,2,3</sup>, Benjamín Rodríguez-Santiago<sup>4</sup>, Aïda Homs<sup>1,2,3</sup>, Javier Santoyo<sup>5</sup>, Maria Rigau<sup>1</sup>, Gemma Aznar-Lain<sup>6</sup>, Miguel del Campo<sup>1,3,7</sup>, Blanca Gener<sup>8</sup>, Elisabeth Gabau<sup>9</sup>, María Pilar Botella<sup>10</sup>, Armand Gutiérrez-Aruri<sup>1,2,3</sup>, Guillermo Antifol<sup>1,3,5</sup>, Luis Alberto Pérez-Jurado<sup>1,2,3</sup>\* and Ivon Cusó<sup>1,2,3</sup>\*



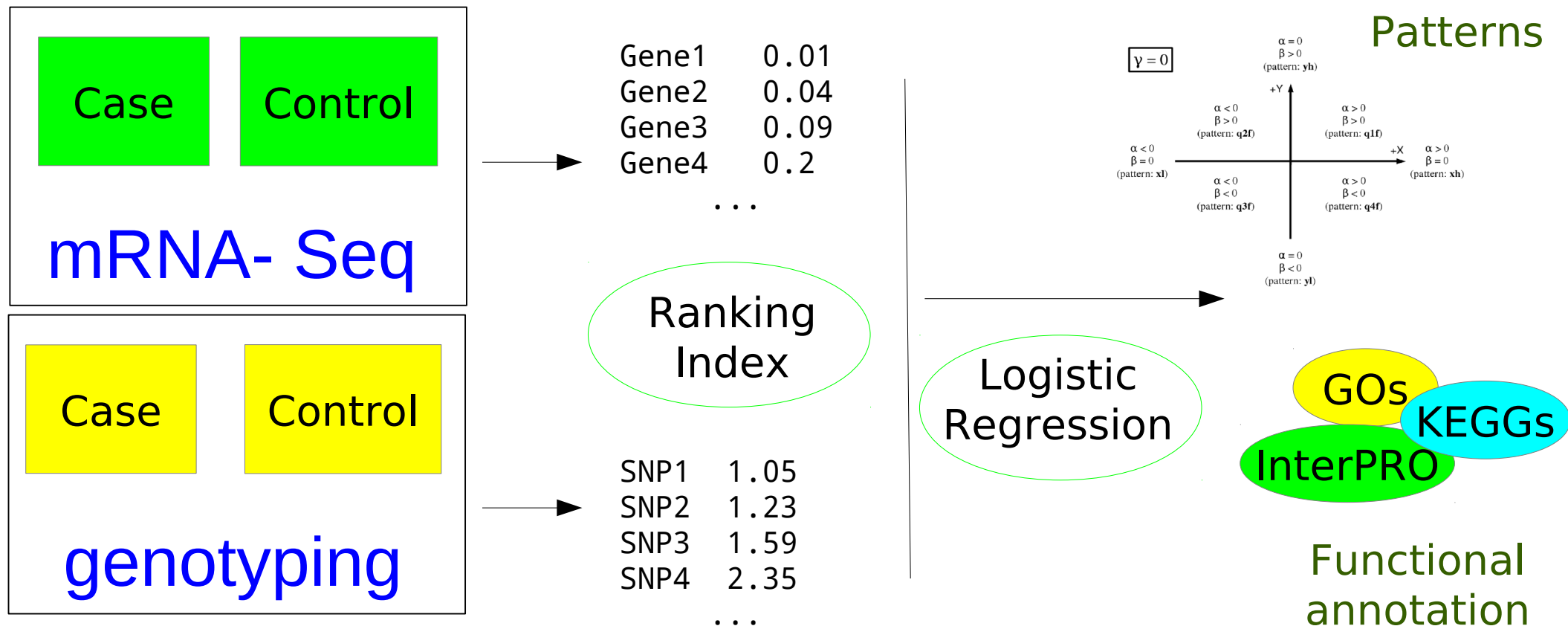
# Multidimensional Gene Set Analysis

## MicroRNA-Seq & mRNA-Seq



# Multidimensional Gene Set Analysis

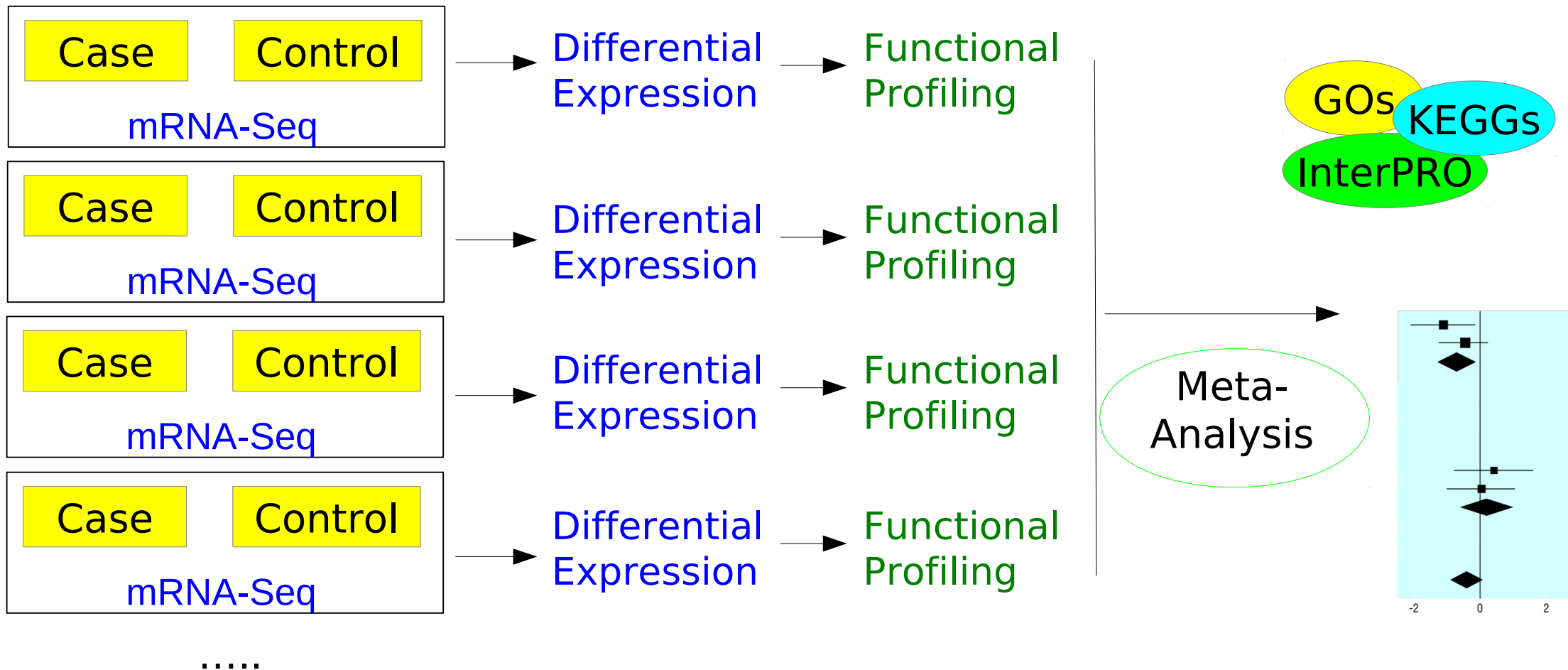
## mRNA-Seq & genotyping association





# Functional Meta-Analysis

## N mRNA-Seq studies

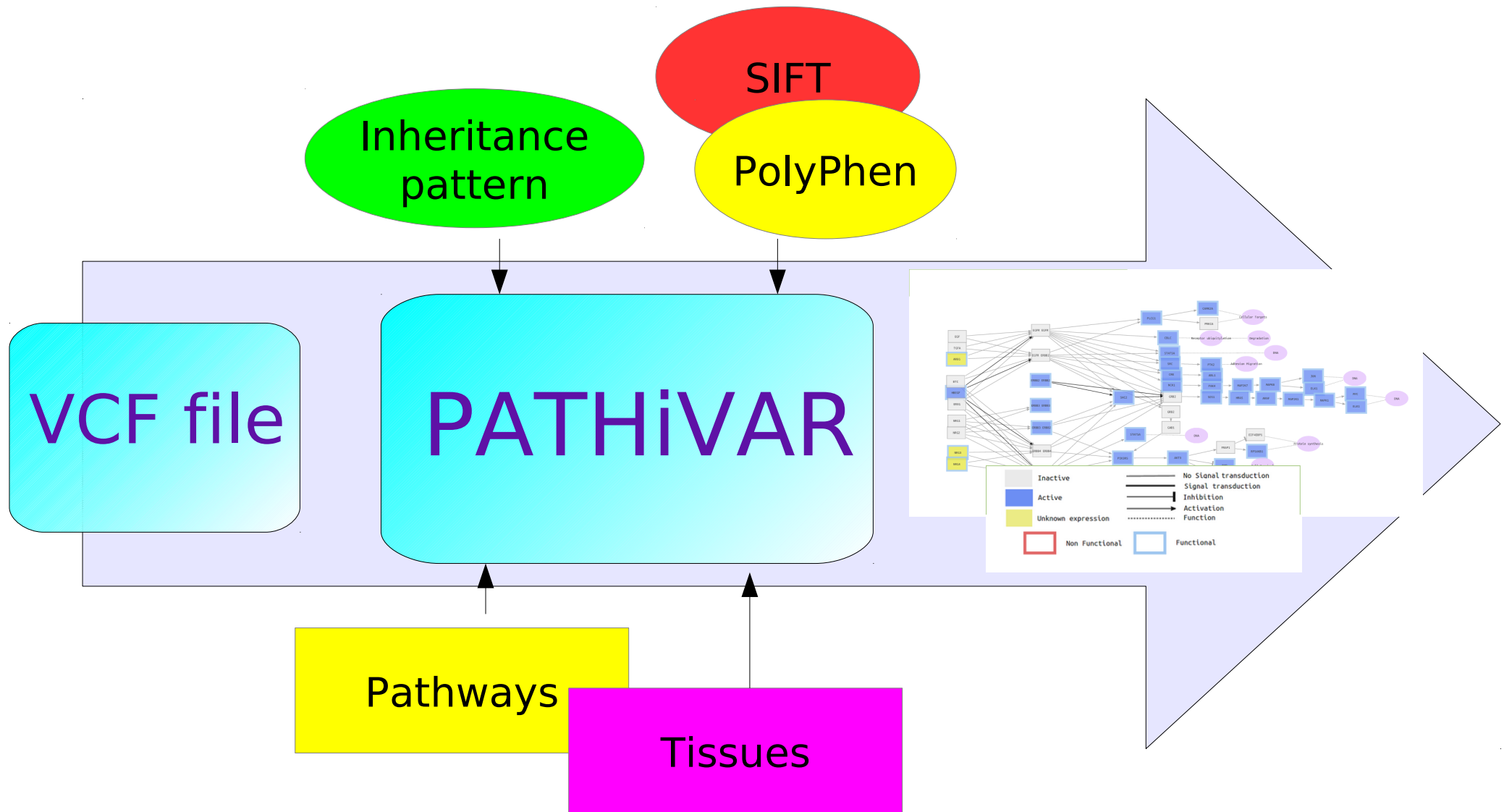


# PATHiVAR: mutations and expression

- **PATHiVAR** estimates the functional impact that mutations have over the human signalling network.
  
- **PATHiVAR:**
  - ▢ Analyses VCF files
  - ▢ Extract the deleterious mutations
  - ▢ Locate them over the signalling pathways in the selected tissue (with the appropriate expression pattern)
  - ▢ Provide a comprehensive, graphic and interactive view of the predicted signal transduction probabilities across the different signalling pathways.

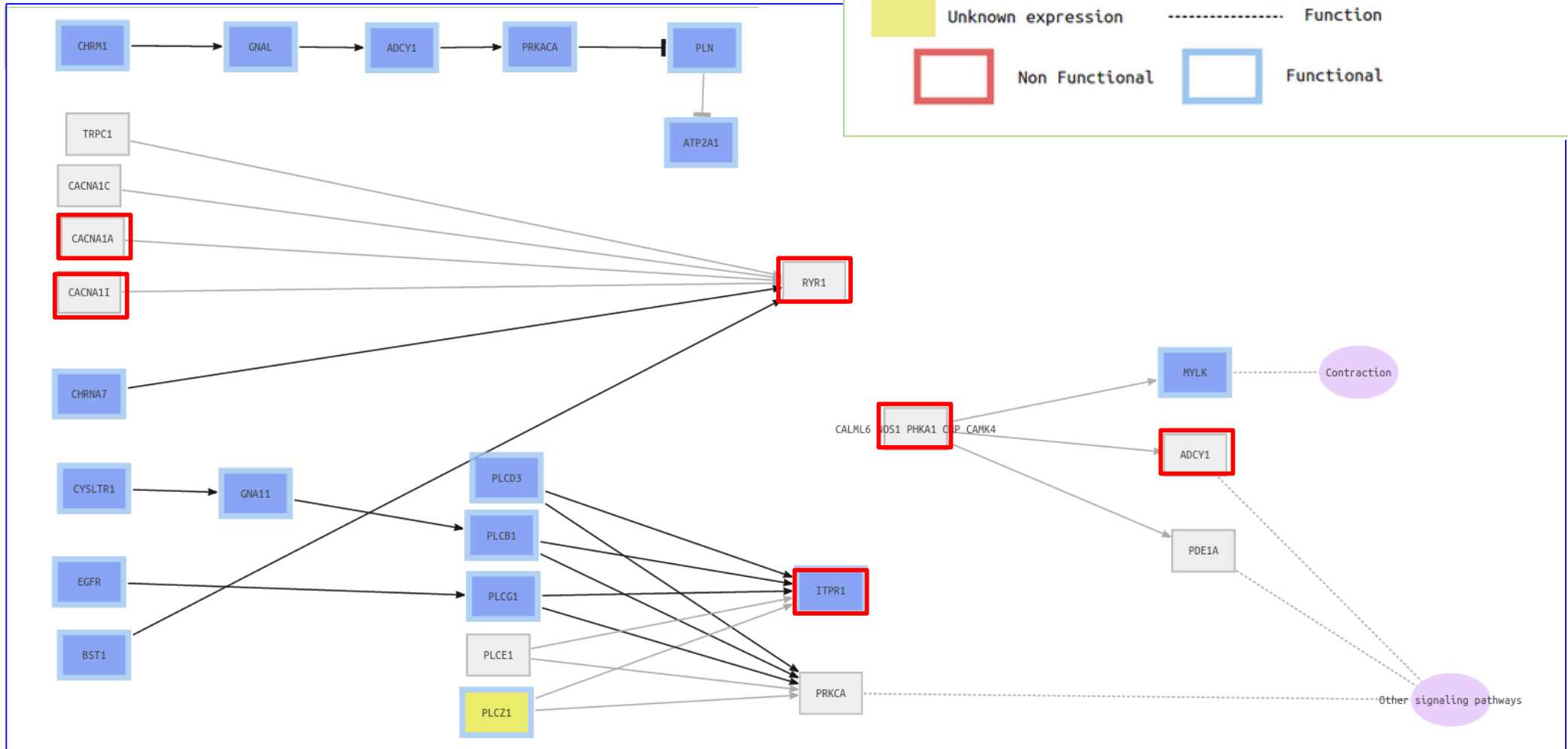
<http://pathivar.babelomics.org/>

# How does PATHiVARK work?



# PATHiVAR

## CALCIUM SIGNALING PATHWAY



# Outline

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- 1) Introduction to NGS Data Analysis
- 2) RNA-Seq Data Analysis
- 3) Resequencing Data Analysis
- 4) Omics Data Integration
- 5) Network Analysis**

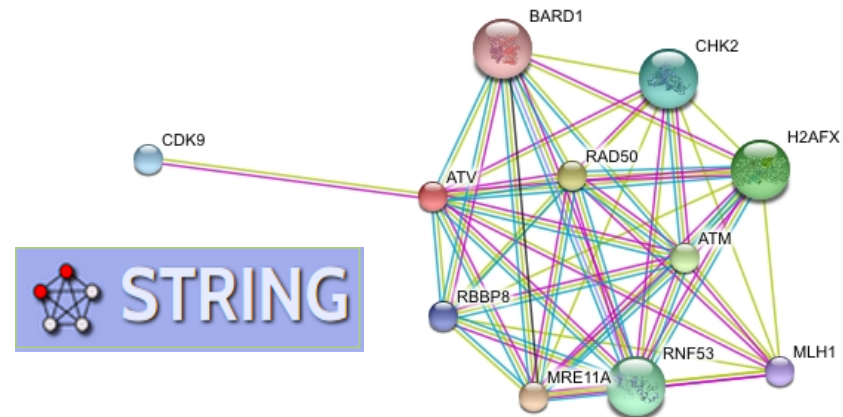
# Protein-Protein Interactions (PPI)

- PPIs are a central point at almost every level of cell function:
  - Structure of subcellular organelles (structural proteins)
  - Packing the chromatin (histones)
  - Protein modifications (kinases)
- Retrieving information about a **single protein**....

5/277 Interacting proteins for BRCA1 (ENSP00000350283<sup>3</sup>)

Interactant		Interaction
GeneCard	External ID(s)	
<a href="#">NBN</a>	<a href="#">ENSP00000265433</a> <sup>3</sup>	STRING (score=.
<a href="#">TOPBP1</a>	<a href="#">ENSP00000260810</a> <sup>3</sup>	STRING (score=.
<a href="#">UBA1</a>	<a href="#">ENSP00000338413</a> <sup>3</sup>	STRING (score=.
<a href="#">UBE2D1</a>	<a href="#">ENSP00000185885</a> <sup>3</sup>	STRING (score=.
<a href="#">GADD45A</a>	<a href="#">ENSP00000360025</a> <sup>3</sup>	STRING (score=.

[About this table](#)



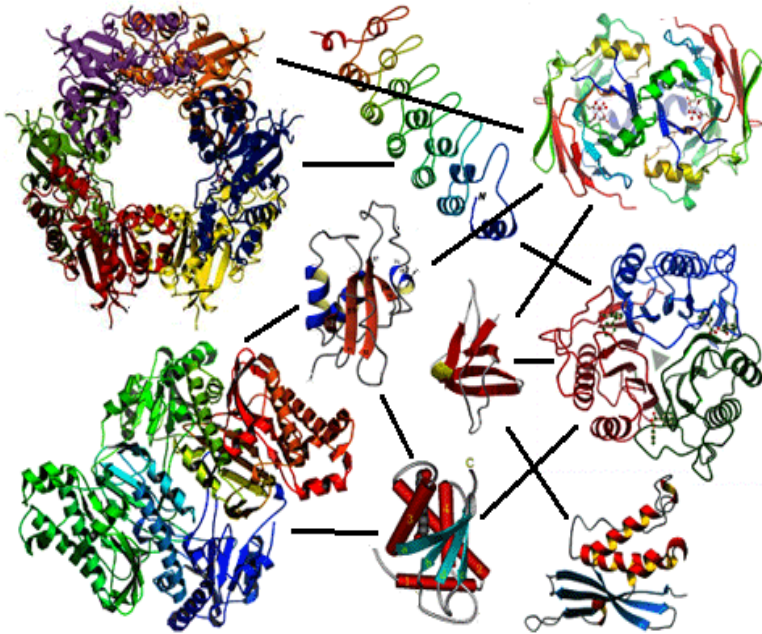
# Protein-Protein Interactions (PPI)

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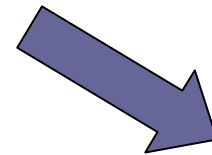
- How to extract information about **sets** of genes?
- How to perform **functional enrichment analysis** using protein-protein interactions as annotation source?
- How to **prioritize candidate genes**?
- How to get **new functional candidate genes**?

# Graph Theory

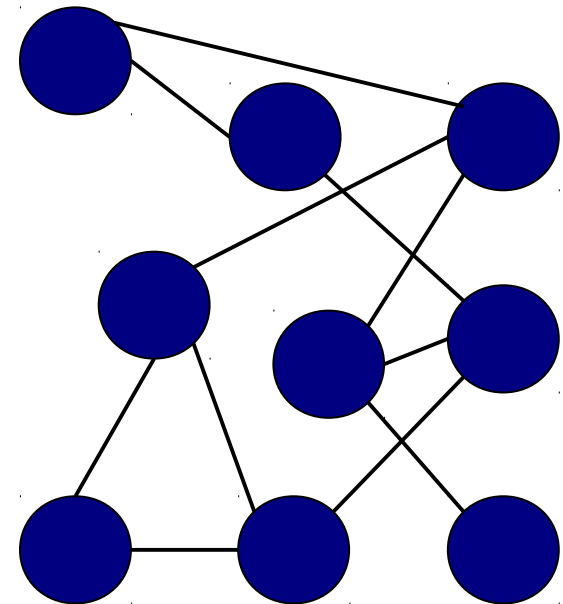
Set of proteins interacting



**Nodes** = proteins  
**Edges** = interaction events



Undirected graph



structured data



# Graph Theory

Graph theory may help us to study protein networks.  
Some interesting parameters:

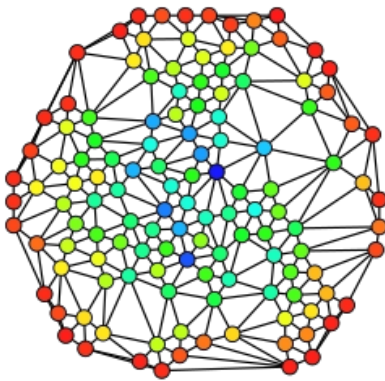
- **Degree (connectivity or connections)**: number of edges connected to a node. Nodes with high degree are called **hubs**.

- **Betweenness**: A measure of centrality of a node, it is defined by:

$$C_B(v) = \sum_{s \neq v \neq t \in V} \frac{\sigma_{st}(v)}{\sigma_{st}}$$

$\sigma_{st}$  is total number of shortest paths in the graph.

$\sigma_{st}(V)$  is the number of shortest paths that pass through node  $V$

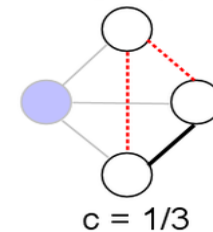


# Graph Theory

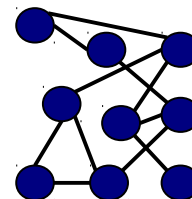
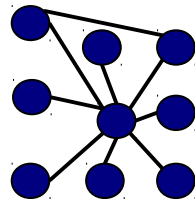
- **Clustering coefficient (of a node)**: A measure of how interconnected the neighbours of that node are. Proportion of links between the nodes within its neighbourhood divided by the number of links that could possibly exist between them.

$$C_i = \frac{2e_i}{n_i(n_i - 1)}$$

$e_i$  is the number of edges among the nodes connected to node  $i$   
 $n_i$  is the number of neighbours of node  $i$



To differentiate between **star-shaped** nets and more **interconnected** nets.



# Graph Theory

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## Some Graph Theory concepts:

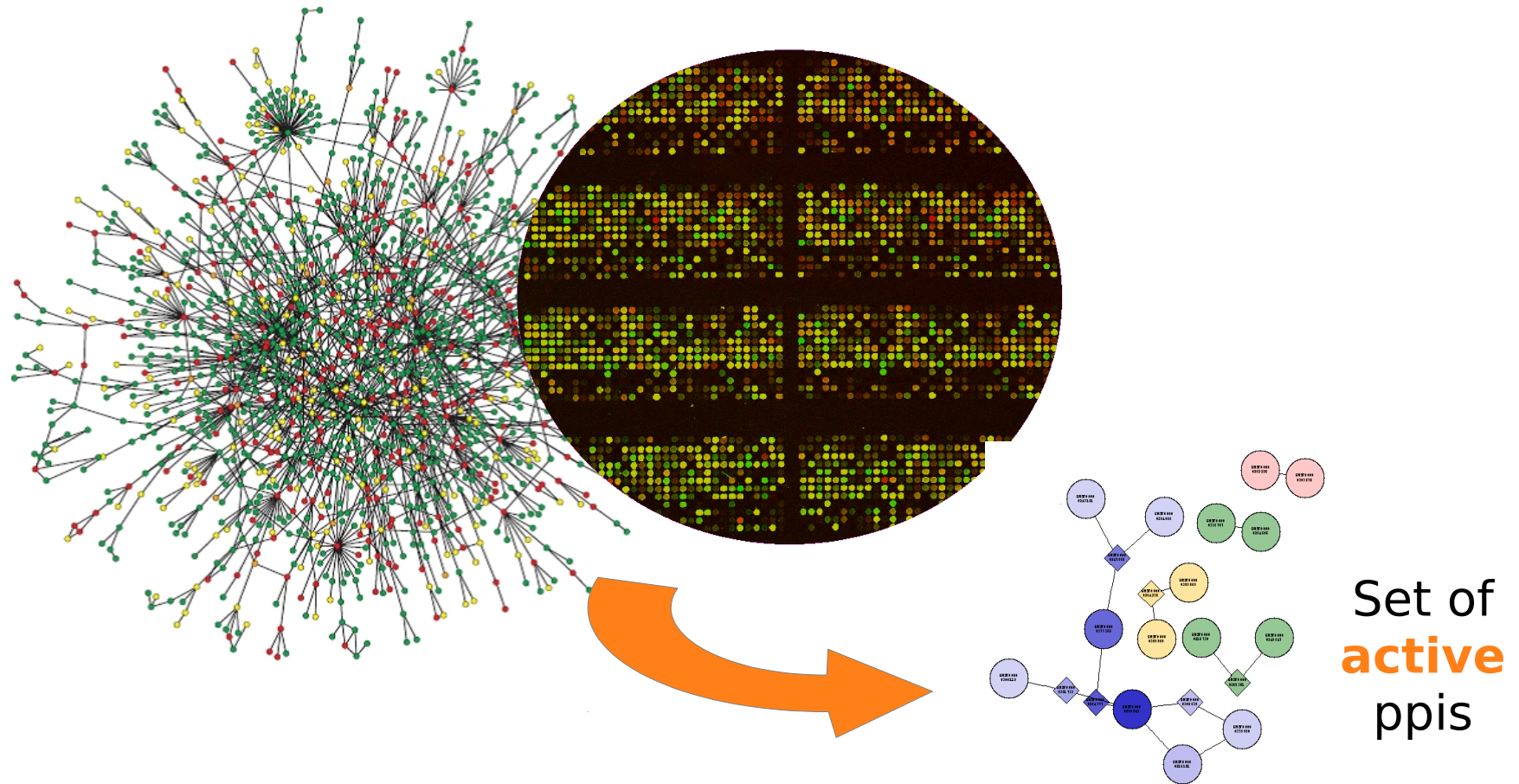
**Shortest path.** The path with less edges that connects two nodes.

**Component.** A group of nodes connected among them.

**Bicomponent.** A group of nodes connected to other group of nodes by only an edge. The edge that joins two bicomponents is called **articulation point**.

# Interactome & Transcriptome

- **Interactome.** Complete collection of protein-protein interactions in the cell.
- **Transcriptome** determines the real interactome.



# Interactome & Transcriptome

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## Goal

To develop a methodology that may **extract from lists of proteins/genes** the ppi networks acting and evaluates whether they have importance in the **cooperative behaviour** of the list.

How we evaluate the cooperative behaviour of a list of proteins/genes in terms of its ppi network parameters?

## Two different approximations

- Importance in **complete interactome**
- Cooperative behaviour - **Minimal Connected Network**



## Babelomics 5

<http://babelomics.bioinfo.cipf.es/>

Functional / Network Enrichment:  
SNOW

# Hands on

There is a well-known list of 72 genes related to eye diseases (ABCA4, ABHD12, ADAMTS18, AIPL1, BBS1, BEST1, C2orf71, C8ORF37, CA4, CABP4, CEP290, CERKL, CHM,...)

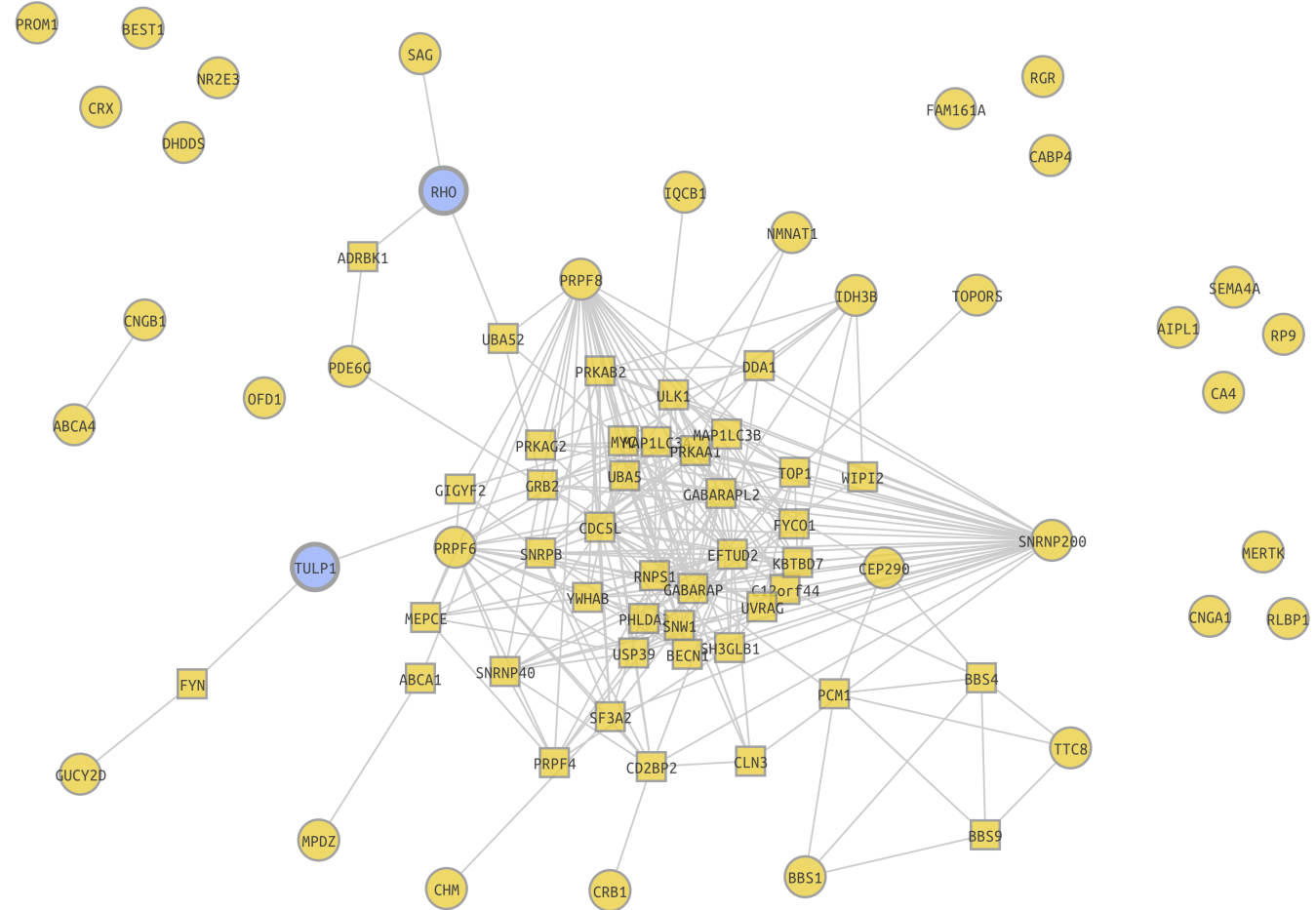
- 1) Now we have a two new candidates: RHO and TULP1 . We would to know what is the relationship between all genes.
- 2) Also it would be interesting to explore new functional candidates.

## **Strategies from Babelomics?**

- Single Enrichment
- **Network** Enrichment

# Hands on

RHO	TULP1
ABCA4	MERTK
ABHD12	MPDZ
ADAMTS18	NMNAT1
AIPL1	NR2E3
BBS1	NRL
BEST1	OFD1
C2orf71	PDE6A
C8ORF37	PDE6B
CA4	PDE6G
CABP4	PRCD
CEP290	PROM1
CERKL	PRPF3
CHM	PRPF31
CLRN1	PRPF6
CNGA1	PRPF8
CNGB1	PRPH2
CRB1	RBP3
CRX	RD3
CYP4V2	RDH12
DHDDS	RGR
EYS	RLBP1
FAM161A	ROM1
FSCN2	RP1
GUCA1B	RP2
GUCY2D	RP9
IDH3B	RPE65
IMPDH1	RPGR
IMPG1	RPGRIP1
IMPG2	SAG
IQCB1	SEMA4A
KCNJ13	SNRNP200
KLHL7	SPATA7
LCA5	TOPORS
LRAT	TTC8
MAK	USH2A





# More info + questions

Nucleic Acids Research Advance Access published May 26, 2014

*Nucleic Acids Research*, 2014 **1**  
doi: 10.1093/nar/gku472

**A web tool for the design and management of panels of genes for targeted enrichment and massive sequencing for clinical applications**

Nucleic Acids Research Advance Access published May 6, 2014

*Nucleic Acids Research*, 2014 **1**  
doi: 10.1093/nar/gku407  
1, 2, 3,\*  
1, and

**A web-based interactive framework to assist in the prioritization of disease candidate genes in whole-exome sequencing studies**

Aleja  
Joaq

Nucleic Acids Research Advance Access published April 20, 2015

*Nucleic Acids Research*, 2015 **1**  
doi: 10.1093/nar/gkv384

**Babelomics 5.0: functional interpretation for new generations of genomic data**

<sup>1</sup>Comp  
<sup>2</sup>Bioinf  
<sup>3</sup>Func

Published online 8 June 2013

*Nucleic Acids Research*, 2013, Vol. 41, Web Server issue **W41–W46**  
doi:10.1093/nar/gkt530

**Genome Maps, a new generation genome browser**

Ignac  
Robe

Nucleic Acids Research Advance Access published April 16, 2015

*Nucleic Acids Research*, 2015 **1**  
doi: 10.1093/nar/gkv349

**Assessing the impact of mutations found in next generation sequencing data over human signaling pathways**

OPEN ACCESS Freely available online

PLoS one

**Multidimensional Gene Set Analysis of Genomic Data**

David Montaner<sup>1,2</sup>, Joaquín Dopazo<sup>1,2,3\*</sup>



**BIER**

**Tutorial:** web tools

# Cursos y colaboraciones

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- Curso CIBERER de análisis de datos genómico, **28-30 Sep 2015** en Valencia.
- Colaboraciones entre grupos CIBER: ayudas de movilidad.
- <http://bioinfo.cipf.es/>